O35690 mus musculu Q6pjd9 homo sapien Aah17199 homo sapi Q6yw21 oryza sativ Bad05688 oryza sat Bad05688 oryza sat Q7syl3 brachydanio Q9h2z4 homo sapien Q9cqm3 mus musculu P97334 mus musculu Q8tau0 homo sapien Q9hah7 homo sapien Q9nah7 homo sapien Q8r089 mus musculu

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21226716; PubMed=11278948; DOI=10.1074/jbc.M011619200;

A Garriga-Canut M., Roopra A., Buckley N.J.;

Garriga-Canut M., Roopra A., Buckley N.J.;

The basic helix-loop-helix protein, SHARP-1, represses transcription

The basic helix-loop-helix protein, SHARP-1, represses transcription

The basic helix-loop-helix protein, SHARP-1, represses transcription

The basic helix-loop-helix protein and histone deacetylase-independent

The basic helix-loop-helix proteins both

The basic land activated transcription.

The basic land activated transcription.
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C 09C0J9;

C 28-FEB-2003 (Rel. 41, Created)

T 28-FEB-2003 (Rel. 44, Last sequence update)

T 28-FEB-2003 (Rel. 44, Last annotation update)

T 05-JUL-2004 (Rel. 44, Last annotation update)

E class B basic helix-loop-helix protein 3 (bHLHB3) (Differentially E expressed in chondrocytes protein 2) (hDEC2) (Enhancer-of-split and E hairy-related protein 1) (SHARP-1).

Name=BHLHB3; Synonyms=DEC2, SHARP1;

Homo sapiens (Human).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21092582; PubMed=11162494; DOI=10.1006/bbrc.2000.4133;
Fujimoto K., Shen M., Noshiro M., Matsubara K., Shingu S., Honda Yoshida E., Suardita K., Matsuda Y., Kato Y.;
Molecular cloning and characterization of DEC2, a new member of helix-loop-helix proteins.";
Biochem. Biophys. Res. Commun. 280:164-171(2001).
                                                                                                                                                                    ALIGNMENTS
               AAH17199
Q6YW21
BAD05688
BAD05845
SIA2_BRARE
NK24_HUMAN
NK24_MOUSE
NK23_HUMAN
FBSH_HUMAN
FBSH_HUMAN
       Q6PJD9
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PIR; JC7583; JC7583.
Genew; HGNC:16617; BHLHB3.
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BHB2_RAT

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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Basic helix-loop-helix domain containing, class B, 3
Name=BHLHB3;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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GO; GO:0003700; F:transcription factor activity;
GO; GO:0030154; P:cell differentiation; NAS.
GO; GO:0008283; P:cell proliferation; NAS.
GO; GO:0009887; P:cell proliferation; NAS.
GO; GO:0006355; P:regulation of transcription, DN InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
DNA-binding; Nuclear protein; Repressor; Transcrip DNA BIND 45 57 Basic motif.
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SEQUENCE 482 AA; 50497 MW; 2BECDC2FDEB7CE14 Cl
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i, 2BECDC2FDEB7CE14 (
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mones on Number S.
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A Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

E MBL; BC025968; AAH25968.1; -.

GO; GO:000357; F:DNA binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA

InterPro; IPR001092; HLH basic.

InterPro; IPR003650; Orange.

R Pfam; PF07527; Hairy orange; 1.

Pfam; PF00010; HLH; 1.

R SMART; SM00353; HLH; 1.

SMART; SM00511; ORANGE; 1.

PROSITE; PS50888; HLH; 1.

SEQUENCE 482 AA; 50525 MW; 23EBD420C6B0CE03 CRC64;
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X MEDLINE=22791403; PubMed=12909371;

X MEDLINE=22791403; PubMed=12909371;

X Wekevova A.V., Aguirre G.D., Acland G.M.;

X Wekevova A.V., Aguirre G.D., Acland G.M.;

X Wekevova A.V., Aguirre G.D., Acland G.M.;

X Cloning and characterization of canine SHARP1 and its evaluation

T "Cloning and characterization of canine SHARP1 and its evaluation

T Gene 312:335-343(2003).

E MBL; AY204567; AAP12464.1; -.

E MBL; AY204568; AAP12465.1; -.

R GO; GO:0006357; F:DNA binding; IEA.

GO; GO:0006357; F:DNA binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA

InterPro; IPR001092; HLH basic.

IN Prom: PF00010; HLH; I.

SMART; SM00353; HLH; I.

SMART; SM00511; ORANGE; 1.

PROSITE; PS50888; HLH; 1.

SAMART; SM00511; ORANGE; 1.

PROSITE; PS50888; HLH; 1.

SQ SEQUENCE 513 AA; 52942 MW; CA7FC23C2E03DCBA CRC64;
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TISSUE=Mammary gland;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy
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Canis.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Bhlhb3 protein (Fragment).
Name=Bhlhb3;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae;
                                                                                                                 Craniata; Vertebrata; Fissipedia; Canidae;
                                                               update)
on update)
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Pred. No. 2.1e-82;
0; Mismatches 0;
                                                    Created)
Last sequence up
Last annotation
                                  513
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                                        O7YQC9;
O1-OCT-2003 (TrEMBLrel. 25, Creat
01-OCT-2003 (TrEMBLrel. 25, Last
05-JUL-2004 (TrEMBLrel. 27, Last
SHARP1 protein.
Name=SHARP1;
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Carnivora; Fi
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Local Similarity 100.0%;
Les 114; Conservative (
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**REDLINE=21092582; PubMed=11162494; DOI=10.1006/bbrc.2000.4133;

**REDLINE=21092582; PubMed=11162494; DOI=10.1006/bbrc.2000.4133;

**Fujimoto K., Shen M., Noshiro M., Matsubara K., Shingu S., Honda K., Fujimoto K., Suardita K., Matsuda Y., Kato Y.;

**Noshida E., Suardita K., Matsuda Y., Kato Y.;

**Molecular cloning and characterization of DEC2, a new member of base in thelix-loop-helix proteins.";

**Legistriction of DEC2, a new member of base in the second in the interpresses bot:

**Legistriction of DEC2, a new member of base in the interpresses in base in the interpresses in base in the interpresses in basic helix-loop-helix (bHLH) domain.

**Legistriction of DEC2, a new member of base in the interpresses in basic helix-loop-helix (bHLH) domain.

**Legistriction of DEC2, a new member of base interpresses in basic helix-loop-helix (bHLH) domain.
        Р.н.,
,k s.w.
                                                              .A.,
Sanchez
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Butterfield
Schein J.
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fatsubara K., Shingu S., Honda
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Murinae; Mu
                               Hulyk
    Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanch Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfiel Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-lengt
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: transcription, DNA-dependent;
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Sciurognathi, Muridae,
Malek J.A.,
iia A.M., Gay
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Class B basic helix-loop-helix protein 3 (bHLHB3)
expressed in chondrocytes protein 2) (mDEC2).
Name=Bhlhb3; Synonyms=Dec2;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                        .s.";
U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81; DB 2; Le
Pred. No. 2.2e-56;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

TISSUE=Mammary gland;
Strausberg R.;
Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ dal
EMBL; BC037742; AAH37742.1; -.
MGD; MGI:1930704; Bhlhb3.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, Dl
InterPro; IPR001092; HLH_basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
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Rodentia;
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100.0%;
                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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81; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 AA;
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Kato Y.;
"Expression of Dec2 -
gene is regulated by
Submitted (NOV-2003)
                                                                                                                                                                                                                                                                              Similarity
81; Conser
                                                                                                                                                                                                                                                410 AA;
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BHLH transcrip
BHLHB3.
Mus musculus (
                                                                                                                                                                                                                                                                                                                                                                                                                                              BAD18970,
20-MAY-2004
20-MAY-2004
                                                                                                                                                                                                                                                                                                               45
                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                               Local
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            collaboration
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P SEQUENCE FROM N.A.

STRAIN=Sprague-Dawley, TISSUE=Cerebellum;

MEDLINE=98193761; PubMed=9532582;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Nol. Cell. Neurosci. 10:460-475(1997).

-1- FUNCTION: May be a transcriptional repressor that represses both basal and activated transcription.

-1- SUBUNIT: Homodimerize.

-1- SUBCELLULAR LOCATION: Nuclear (By similarity).

-1- TISSUE SPECIFICITY: Highly expressed in subregions of the brain, moderately expressed in skeletal muscle, heart. Weakly expressed
                                                                                                                                                                                                              regulation.
                                                                                                                                                                                                                                                                                                                                kartus norvegicus (kat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; R
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                                                                                                                                                                                                            Transcription
                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                               SULT 6
B3_RAT
BHB3_RAT
STANDARD; PRT; 410 AA.
035779;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
class B basic helix-loop-helix protein 3 (bHLHB3) (Eand hairy-related protein 1) (SHARP-1).
Name=Bhlhb3; Synonyms=Sharp1;
                                                                                                                                                                                                          Repressor; Transcript:
Basic motif.
Helix-loop-helix motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shown
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4e-56;
0;
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                                                                                                                                                                                                                                           Orange.
Ala/Gly-rich.
40A87281B08E233D
                                                                                                                                                                                                                                                                                     Score 81; DB Pred. No. 4e-80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             125
                                                                                    EMBL; AB044090; BAB21503.1; -. PIR; JC7584; JC7584.

MGD; MGI:1930704; Bhlhb3.

InterPro; IPR001092; HLH basic.

InterPro; IPR003650; Orange.

Pfam; PF00010; HLH; 1.

SMART; SM00353; HLH; 1.

SMART; SM00511; ORANGE; 1.

PROSITE; PS50888; HLH; 1.

DNA-binding; Nuclear protein; Red DOMAIN

45 57 Bai

DOMAIN

129 175 Ore
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A basic.
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TEQQHQKIIALQNGERSLKSP
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58
129
321
410 AA;
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                                                                                                                                                                                                                                                                SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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a molecular clock system.";
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulation.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musin
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Hamaguchi H., Fujimoto K., Kawamoto T., Noshiro M., Maemura K.,
Takeda N., Nagai R., Furukawa M., Honma S., Honma K., Kurihara
Kato Y.;
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Ala/Gly-rich.
829705CA3A013127 CRC64;
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Basic motif.
Helix-loop-helix motif.
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SEQUENCE FROM N.A.
PubMed=11162494;
Fujimoto K., Shen M., Noshiro M., Matsubara K., Yoshida E., Suardita K., Matsuda Y., Kato Y.;
"Molecular cloning and characterization of DEC2, helix-loop-helix proteins.";
Biochem. Biophys. Res. Commun. 280:164-171(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
4e-56;
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RGD; 70900; Bhlhb3.
InterPro; IPR001092; HLH_basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy_orange; 1.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
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Kato Y., Honma K.;
"Decl and Dec2 are regulators
Nature 419:841-844(2002).
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DNA-binding; Nuclear pro
DNA BIND 45 57
DOMAIN 129 175
DOMAIN 321 344
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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Antiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J. Generation and initial analysis of more than 15,000 full-length B. M. "Generation and initial analysis of more than 15,000 full-length)
                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:76913.
Name=zgc:76913;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniforr Cyprinidae; Danio.
NCBI_TaxID=7955;
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            CRC64;
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d. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 9.3e-34;
0; Mismatches 0;
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                                  Score 81; DB
Pred. No. 4e-
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InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
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TISSUE=Kidney;

MEDLINE=22388257; PubMed=12477932;

A Reusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzratne P.H.,
A Blakesley S.J., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Diess S.J., Maria M.A.;
A Jones S.J., Maria M.A.;
A Jones S.J., Maria M.A.;
A mouse cDNA sequences.",
R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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la; Pipoidea;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
. protein zgc:76913.
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Pred. No. 9.3e-34;
0; Mismatches 0;
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OGGNE9;

OS-JUL-2004 (TrEMBLrel. 27, Created)

OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)

OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Hypothetical protein (Fragment).

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Kenopus laevis (African clawed frog).

Kenopus laevis (African clawed frog).

Amphibia; Metazoa; Chordata; Craniata; Vertel Amphibia; Piles
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Submitted (MAR-2004) to the
EMBL; BC066738; AAH66738.1;
Hypothetical protein.
SEQUENCE 403 AA; 44682 MW
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ZGC:76913.
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SEQUENCE FROM N.A.

TISSUE=21388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marunina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marunina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marunina K., Farmer A.A., Rubin G.M., Hong L.,

RA Bloaks S.A., Doquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boak S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunnarathe P.H.,

RA Boak S.S., Morley K.C., Hale S., Garcia A.M., Gabb R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mitting M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Schrinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length huma

RT

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                     human
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S.G.,
S.W.,
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                       11132; PubMed=12454917;
Strausberg R.L., Wagner L., Pontius J., Clifton S.W
                                                                                                                                                                                                                                                                                                                                                                          research: The NIH Xenopu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B2) (Stimulated (eipl).
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[3]
SEQUENCE FROM N.A.
TISSUE=Spleen;
Klein S., Strausberg R.;
Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073563; AAH73563.1; -.
InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EECF92EC6845B0D7 CRC64;
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BHBZ_MOUSE
STANDARD; PKI; JI f....
BHBZ_MOUSE
035185; P97289;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Class B basic helix-loop-helix protein 2 (bHLHB2) (Streingle acid 13) (E47 interaction protein 1) (eipl)
Name=Bhlhb2; Synonyms=Strai3, Clast5;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 2; Le
Pred. No. 9.4e-34;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                      TISSUE=Spleen;
MEDLINE=22341132; PubMed=1245;
Klein S.L., Strausberg R.L., Richardson P.;
"Genetic and genomic tools foinitiative.";
Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45446 MW;
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Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100
53; Conservative
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Xenopodinae; Xenopus
NCBI_TaxID=8355;
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EMBL outstation
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TISSUE-Adammary gland;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Groues L.H., Derge J.G., Schuler G.D.,
Altechul S.F., Zeeberg B., Wagner L., Schaefer C.F., Bhat N.K.,
Altechul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Altechul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
A piachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B capteron M.J., Ordan H., Moore T., Max S. I., Wang J., Histeh F. S.

B chapteron M.J., Ordan H., Moore T., Mark J.A., Rubin G.M., Hong L.,
B charter S.F., Logdelland N.A., Peters G.J., Abramon R.D., Mullay S.J.,
B chards S.A., McEvana P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
B chards S., Worley K.C., Hale S. Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.X., Muzny D.M., Sodergren B.J., Lux X., Gibbas R.A.,
B chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.X., Muzny D.W., Sodergren B.D., Dickson M.C.,
B chards S.W., Touchman U.W., Green E.D., Dickson M.C.,
B Schnerch A., Schin J.B., Young S.J. M., Marz M.A.,
B chard Y.S.N., Krzywinski M.I., Stalska U., Smailus D.E.,
Marting M., Madan A., Jones S.J.M., Marz M.A.,
B chard Y.S.N., Krzywinski M.I., Stalska U., Smailus D.E.,
B cheration and initial analysis of more than 15,000 full-length human constitution and initial analysis of more than 15,000 full-length human constitution as a transcriptional factor for neuronal differentiation J.B., Nones S.J.M., Marz M.A.,
C --- SUBNIT Able to homodimerize or heterodimerize with E47.
C --- SUBNIT Able to homodimerize or heterodimerize with E47.
C --- SUBNIT Able to homodimerize or heterodimerize with E47.
C --- SUBNIT Able to homodimerize or heterodimerize with E47.
C --- SUBNIT Able S.B. Styressed from E9:5 day to E17:5 day in the vertinal pigment epithelium, developing eyelids, has all epithelium, events and urchina Paran and urchina epithelium, developing eyelide, has a pointer a serous gland, vibrisae, epithelium of the mound epithelium of the sop
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"Identification of interaction partners for the basic-helix-loop-helix
                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND INTERACTION WITH E47/TCF3.
STRAIN=BALB/c;
MEDLINE=97203270; PubMed=9050988; DOI=10.1038/sj.onc.1200912;
Dear T.N., Hainzl T., Follo M., Nehls M., Wilmore H., Matena K.,
                                                                                                                                                                         ible gene
promotes
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                                                                                                                                                                     "Overexpression of Stra13, a novel retinoic acid-inducible basic helix-loop-helix family, inhibits mesodermal and proneuronal differentiation of P19 cells.";
Genes Dev. 11:2052-2065(1997).
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                                                                                                          Bouillet
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                                                               PubMed=9284045;
ja R., Matsubara
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5; TISSUE=Spleen;
                                    carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein E47.";
Oncogene 14:891-898(1997)
SEQUENCE FINCTION TISSUE=Embryonic carcinow MEDLINE=97427857; PubMed=
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SEQUENCE FROM N.F
STRAIN=C57BL/6; 7
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"Isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein E47."
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05-JUL-2004 (T
05-JUL-2004 (T
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Name=SHARP-2;
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ID BAD01588
AC BAD01588;
DT 02-MAR-2004
DT 02-MAR-2004
    an
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Matches 52
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PROSITE;
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C 035780;
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 44, Last annotation update)
T 28-FEB-2004 (Rel. 44, Last annotation update)
T 05-JUL-2004 (Rel. 44, Last annotation update)
T 08-FEB-2003 (Rel. 44, Last annotation update)
T 08-FEB-2004 (Rel. 44, Last annotation update)
T 18-FEB-2004 (Rel. 44, Last annotation update)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE Sprague-Dawley; TISSUE=Hippocampus;

A Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;

L. SHBLORI SECONTION: Uctor as a transcriptional factor for neuron differentiation.

C. -!- SUBCULITAR LOCATION: Nuclear (By similarity).

C. -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

C. -!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung, liver, muscle, kidney, uterus and gut.

C. -!- TISSUE SPECIFICITY: Contains 1 basic helix-loop-helix (bHLH) domain.

C. -!- SIMILARITY: Contains 1 brasic helix-loop-helix (bHLH) domain.

C. -!- SIMILARITY: Contains 1 orange domain.

C. -!- SIMILARITY: Contains 1 orange domain.

C. -!- SIMILARITY: Contains 1 orange domain.
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                EMBL; AF010305; AAB64228.1; -.

EMBL; AF010305; AAB64228.1; -.

EMBL; AF364051; AAK50859.1; -.

EMBL; BC010720; AAH10720.1; -.

EMBL; BC010720; AAH10720.1; -.

EMBL; BC010720; AAH10720.1; -.

MGD; MGI:1097714; Bhlbb2.

GO; GO:0005634; C:nucleus; IDA.

GO; GO:000564; F:transcriptional repressor activity; IDA.

GO; GO:0016564; F:transcription of transcription, DNA-d..

EN Fam; PF0011092; HLH basic.

Fram; PF00110; HLH; I.

FROSITE; PS50888; HLH; I.

FROMAIN 140 184 Orange.

CONFLICT 288 288 K -> T (in Ref. 2).

SEQUENCE 411 AA, 45360 MW; B392893CD49292BC CRC64;
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Murinae; Rattus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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split-and hairy-related protein-2.
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TISSUE=Kidney;

PubMed=14725860;

Hirano S., Yamada K., Kawata H., Shou Z., Mizutar Mayumi M., Miyamoto K.;

"The rat enhancer of split- and hairy-related proexpression, genomic structure, and promoter analy Arch. Biochem. Biophys. 422:81-90(2004).

EMBL; AB096137; BAD01588.1; -.

InterPro; IPR001092; HiH basic.

InterPro; IPR003650; Orange.

Pfam; PF07527; Hairy orange; 1.

Pfam; PF00010; HiH; 1.

SMART; SM00353; HiH; 1.
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Pred. No. 5.9e-33;
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             RGD; 68439; Bhlhb2.
InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
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                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
16 days embryo head cDNA, RIKEN full-length enriched library,
clone:Cl30042M06 product:basic helix-loop-helix domain containing,
class B2, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           class B2, full insert sequence.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the FANTOM Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
"Analysis of the Mouse transcriptome based on functional
Nature 420:563-573(2002).
[2]
                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                          2086DABB3DB82058 CRC64;
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TISSUE=Kidney;
Hirano S., Yamada K., Kawata H., Shou Z., Mizuta Mayumi M., Miyamoto K.;
"The rat enhancer of split- and hairy-related prexpression, genomic structure, and promoter anal Arch. Biochem. Biophys. 422:81-90(2004).
EMBL; AB096137; BAD01588.1; -.
SEQUENCE 411 AA; 45557 MW; 2086DABB3DB82058
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(TrEMBLrel. 27, Last annotation split-and hairy-related protein-
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA c1"
"Ather Fravmol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-1
Nature 409:685-690(2001).
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100.0%;
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STRAIN=C57BL/6J; TISSUE=Head;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK048242; BAC33281.1; -.
SEQUENCE 411 AA; 45360 MW; B392893CD49292BC CRC64;
P SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Head;

K STRAIN=C57BL/6J; TISSUE=Head;

K Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Ronno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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ALIGNMENTS

| differentiation and proliferation. The pre   | development of drugs for the treatment and prevention of involving cell differentiation and proliferation. The pre   | transcription factor designated DEC2. DEC2 can be used as a tool development of drugs for the treatment and prevention of disorder   | The present invention describes a basic helix loop helix (bHLH) t  |
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| The present invention describes a basic helix loop helix (bHLH) t<br>transcription factor designated DEC2. DEC2 can be used as a tool  | The present invention describes a basic helix loop helix (bHLH) transcription factor designated DEC2. DEC2 can be used as a tool   | The present invention describes a basic helix loop helix (bHLH) t  |  |
| Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix (bHLH) t transcription factor designated DEC2. DEC2 can be used as a tool development of drugs for the treatment and prevention of disorder   | Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix (bHLH) transcription factor designated DEC2. DEC2 can be used as a tool   | Claim 2; Page 69-72; 83pp; Japanese.<br>The present invention describes a basic helix loop helix (bHLH) t  | Claim 2; Page 69-72; 83pp;   |
| and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix (bHLH) t transcription factor designated DEC2. DEC2 can be used as a tool development of drugs for the treatment and prevention of disorder   | and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix (bHLH) transcription factor designated DEC2. DEC2 can be used as a tool   | and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix (bHLH) t  |  |
| development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix transcription factor designated DEC2. DEC2 can be used a development of drugs for the treatment and prevention of   | development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix transcription factor designated DEC2. DEC2 can be used a factor of drugs for the transcription factor designated DEC2.  | development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix   | development of drugs for treatment of disorders of cell<br>and proliferation.<br>Claim 2; Page 69-72; 83pp; Japanese.  |
| DEC2 is a basic helix loop helix protein of the DEC fami development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix transcription factor designated DEC2. DEC2 can be used a development of drugs for the treatment and prevention of drugs for the treatment and prevention of  | DEC2 is a basic helix loop helix protein of the DEC family for us development of drugs for treatment of disorders of cell different and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix (bHLH) t transcription factor designated DEC2. DEC2 can be used as a tool   | DEC2 is a basic helix loop helix protein of the DEC fami development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix  | DEC2 is a basic helix loop helix protein of the DEC fami<br>development of drugs for treatment of disorders of cell<br>and proliferation.<br>Claim 2; Page 69-72; 83pp; Japanese.  |
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| HUGAI SEIYAKU KK.  C, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  It invention describes a basic helix loop helix ion factor designated DEC2. DEC2 can be used a for the treatment and prevention of   | HUGAI SEIYAKU KK.  C, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC famint of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  It invention describes a basic helix loop helix ion factor designated DEC2. DEC2 can be used a factor designated DEC2.   | HUGAI SEIYAKU KK.  K, Shin M, Kato Y;  L202935/20.  AF74776.  basic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  | HUGAI SEIYAKU KK.  C, Shin M, Kato Y;  L202935/20.  AF74776.  basic helix loop helix protein of the DEC famint of drugs for treatment of disorders of cell teration.  Page 69-72; 83pp; Japanese.  |
| 10; 2000WO-JP003991.  19; 99JP-00233286.  10GAI SEIYAKU KK.  1. Shin M, Kato Y;  1. Shin M, Kato Y;  202935/20.  1. AF74776.  1. Saic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  1. Sage 69-72; 83pp; Japanese.  1. Invention describes a basic helix loop helix ion factor designated DEC2. DEC2 can be used a for the treatment and prevention of   | 10; 2000WO-JP003991.  19; 99JP-00233286.  10GAI SEIYAKU KK.  4, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC famint of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  1t invention describes a basic helix loop helix ion factor designated DEC2. DEC2 can be used a factor designated DEC2.   | 100; 2000WO-JP003991.  199; 99JP-00233286.  10GAI SEIYAKU KK.  4, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC famint of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  1t invention describes a basic helix loop helix  | 10; 2000WO-JP003991.  19; 99JP-00233286.  1UGAI SEIYAKU KK.  4, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC famint of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.   |
| 01.  00; 2000WO-JP003991.  99; 99JP-00233286.  HUGAI SEIYAKU KK.  4, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC family tof drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  ht invention describes a basic helix loop helix ion factor designated DEC2. DEC2 can be used and prevention of the freatment and prevention of   | 11.  10.; 2000WO-JP003991.  19.; 99JP-00233286.  1UGAI SEIYAKU KK.  1. Shin M, Kato Y;  202935/20.  202935/20.  Lesic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  1t invention describes a basic helix loop helix for designated DEC2. DEC2 can be used of the display of discorders of the display of the | 01.  00; 2000WO-JP003991.  19; 99JP-00233286.  10GAI SEIYAKU KK.  4, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  1t invention describes a basic helix loop helix   | 01. 00; 2000WO-JP003991. 09; 99JP-00233286. IUGAI SEIYAKU KK.  C, Shin M, Kato Y;  L202935/20. AF74776. basic helix loop helix protein of the DEC famint of drugs for treatment of disorders of cell feration. Page 69-72; 83pp; Japanese.   |
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| ix loop helix protein; cell differentiation; prens.  51-A1.  51-A1.  90; 2000WO-JP003991.  90; 99JP-00233286.  40; Shin M, Kato Y;  4202935/20.  4874776.  basic helix loop helix protein of the DEC family tof drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  1t invention describes a basic helix loop helix ton factor designated DEC2. DEC2 can be used and prevention of drugs for the treatment and prevention of the free femily and prevention of the femily and prevention of th | ix loop helix protein; cell differentiation; prens. 51-A1. 51-A1. 50; 2000WO-JP003991. 59; 99JP-00233286. 40; Shin M, Kato Y; 4. Shin M, Kato Y; 5202935/20. 5774776. 583pp; Japanese. 58ge 69-72; 83pp; Japanese. 69ge 69-72; 83pp; Japanese. 61 invention describes a basic helix loop helix lon factor designated DEC2 can be used in the factor designated DEC2. DEC2 can be used in the factor designated DEC2.   | ix loop helix protein; cell differentiation; prens. 51-Al. 51-Al. 50; 2000WO-JP003991, 50; 99JP-00233286. 59; 99JP-00233286. 47, Shin M, Kato Y; 47,776. 47,776. 5202935/20. 5 | ix loop helix protein; cell differentiation; prens.  51-A1.  51-A1.  50; 2000WO-JP003991.  59; 99JP-00233286.  TUGAI SEIYAKU KK.  K, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  |
| DEC2a; DEC2b; bHLM type transcription factor; DEC2; DEC3 basic helix loop helix protein; cell differentiation; protein sapiens.  WO200114551-A1.  01-MAR-2001.  19-JUN-2000; 2000WO-JP003991.  19-JUN-2000; 2000WO-JP003991.  19-AUG-1999; 99JP-00233286.  (CHUS) CHUGAI SEIYAKU KK.  Fujimoto K, Shin M, Kato Y;  WPI; 2001-202935/20.  N-PSDB; AAF74776.  DEC2 is a basic helix loop helix protein of the DEC fami development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix transcription describes designated DEC2 can be used a development of drugs for the treatment and prevention of drugs of the prevention of drugs for the treatment and drugs for the tr | DEC2a; DEC2b; bHLM type transcription factor; DEC2; DEC3 basic helix loop helix protein; cell differentiation; proteins appiens.  WO200114551-A1.  01-MAR-2001.  19-JUN-2000; 2000WO-JP003991.  19-JUN-2000; 2000WO-JP003991.  19-AUG-1999; 99JP-00233286.  (CHUS) CHUGAI SEIYAKU KK.  Fujimoto K, Shin M, Kato Y;  WPI; 2001-202935/20.  N-PSDB; AAF74776.  DEC2 is a basic helix loop helix protein of the DEC fami development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix transcription factor designated DEC2 can be used a basic beliam of the present invention describes a basic helix loop helix transcription factor designated DEC2. DEC2 can be used a basic beliam of the present invention describes a basic helix loop helix transcription factor designated DEC2. DEC2 can be used a basic beliam of the present invention describes a basic helix loop helix transcription factor designated DEC2. DEC2 can be used a basic beliam of the limitation factor designated DEC2. DEC2 can be used a basic beliam of the limitation factor designated DEC2. DEC2 can be used a basic beliam of the limitation factor designated DEC2. DEC2 can be used a basic beliam of the limitation factor designated DEC2. DEC2 can be used a basic beliam of the limitation factor designated DEC2. DEC2 can be used a basic beliam of the limitation of the limitati | DEC2a; DEC2b; DHLH type transcription factor; DEC2; DEC1 basic helix loop helix protein; cell differentiation; pr Homo sapiens.  WO200114551-A1.  01-MAR-2001.  19-JUN-2000; 2000WO-JP003991.  19-AUG-1999; 99JP-00233286.  (CHUS) CHUGAI SEIYAKU KK.  Fujimoto K, Shin M, Kato Y;  WPI; 2001-202935/20.  N-PSDB; AAF74776.  DEC2 is a basic helix loop helix protein of the DEC fami development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.  The present invention describes a basic helix loop helix   | DEC2a; DEC2b; DHLH type transcription factor; DEC2; DEC1 basic helix loop helix protein; cell differentiation; proteins.  WO200114551-A1.  01-MAR-2001.  19-JUN-2000; 2000WO-JP003991.  19-AUG-1999; 99JP-00233286.  (CHUS ) CHUGAI SEIYAKU KK.  Fujimoto K, Shin M, Kato Y;  WPI; 2001-202935/20.  N-PSDB; AAF74776.  DEC2 is a basic helix loop helix protein of the DEC fami development of drugs for treatment of disorders of cell and proliferation.  Claim 2; Page 69-72; 83pp; Japanese.   |
| 2b protein sequence SEQ ID NO:12.  22b; bHLH type transcription factor; DEC2; DEC1  ix loop helix protein; cell differentiation; prens.  51-A1.  51-A1.  50; 2000WO-JP003991.  59; 99JP-00233286.  K, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  tinvention describes a basic helix loop helix in factor designated DEC2. DEC2 can be used a for the freatment and prevention of the office of the freatment and prevention of the office of the freatment and prevention of the office of the office of the freatment and prevention of the office of the office of the office of the freatment and prevention of the office of the of | 2b protein sequence SEQ ID NO:12.  22b; bHLH type transcription factor; DEC2; DEC1  ix loop helix protein; cell differentiation; prens.  51-A1.  51-A1.  50; 2000WO-JP003991.  59; 99JP-00233286.  40GAI SEIYAKU KK.  7, Shin M, Kato Y;  7, Shin M, Kato Y;  202935/20.  AF74776.  basic helix loop helix protein of the DEC family of drugs for treatment of disorders of cell feration.  Page 69-72; 83pp; Japanese.  1t invention describes a basic helix loop helix in factor designated DEC2 can be used in the factor of disorders of cell in the factor of disorders of cell in the factor designated DEC2 can be used in the factor of disorders.   | 2b protein sequence SEQ ID NO:12.  22b; bHLH type transcription factor; DEC2; DEC1  Ex loop helix protein; cell differentiation; prens.  51-A1.  51-A1.  50; 2000WO-JP003991.  59; 99JP-00233286.  40GAI SEIYAKU KK.  4, Shin M, Kato Y;  5, Shin M, Kato Y;  5, Shin M, Kato Y;  5, Shin M, Kato Y;  6, Shin M, Kato Y;  702935/20.  77776.  basic helix loop helix protein of the DEC familiate of disorders of cell derugs for treatment of disorders of cell derugs for treatment of disorders of cell deruge 69-72; 83pp; Japanese.   | 2b protein sequence SEQ ID NO:12.  12b; bHLH type transcription factor; DEC2; DEC1  1x loop helix protein; cell differentiation; prens.  11-A1.  10; 2000WO-JP003991.  10; 2000WO-JP0033286.  10; 2000WO-JP0033286.  10; 2000WO-JP0033286.  10; 2000WO-JP0033286.  10; 2000WO-JP003991.  10; 2 |
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Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
       The present invention describes a basic helix loop helix (bHLH) type transcription factor designated DEC2. DEC2 can be used as a tool in the development of drugs for the treatment and prevention of disorders involving cell differentiation and proliferation. The present sequence represents the specifically claimed human DEC2a protein, as given in the present invention
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                                                                                                                                   Similarity 100.0%; In Conservative 0;
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                                                                   LLTQQVPLSKGTGAPSAAGSAAAPCLERAGQKLEPLAYCVPVIQRTQPSAELAA
            cloop helix protein of the for treatment of disorders
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N-PSDB; AAF74767.
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The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determini whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the
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e disease, comprises c
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A, Vieby
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Olandt PJ, Sen A,
RE, Zhao X, Glatt
                                                                                                                                                                                                                                                                                                                               Assessing whether a patient is afflicted with assessing the stage or progression of the disthe expression level of a cancer marker in a from a non cancer patient.
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2001US-0276025P.
2001US-0276026P.
2001US-0311732P.
2001US-0323580P.
2001US-0325102P.
2001US-0325102P.
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Morrisey MP, Olas
1 K, Schmandt RE,
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N-PSDB; ABS76400.
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10-AUG-2001;
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                                                                                                                                                                                                                                                    Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis; lung disease; emphysema; obstructive pulmonary disease; haemophilia; stroke; infection.
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3 C, Rothenberg ME, Guo
1 R, Ji W, Miller CE;
Padigaru M, Alsobrook JE
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Kekuda l
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Ellerman K,
Catterton E,
Shenoy SG, I
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2001US-0318130P.
2001US-0328430P.
2001US-0322636P.
2001US-0322816P.
2001US-0322817P.
2001US-0323813P.
2001US-0323636P.
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2001US-0324969P.
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Vernet CAM,
, Leach MD, C
Taupier RJ, S
Edinger SR, B
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N-PSDB; ACD19338.
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The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polymucleotide is useful for treating endocrine/ metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. poscriasis, allergy, lupus erythematosus, asthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (eng. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of drugs during clinical trials. This is the amino acid sequence of a novel human NOV protein
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The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; a method of detecting invention by against a polypeptide of the invention; and methods of invention detecting invention further dissolves methods for polypeptides of the invention; and methods of invention further dissolves methods for polypeptides of peventing, treating or amoliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention of ADC33269 ADC33281. The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of date and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's diseases and other neurodegemerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers,
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                                                                                                                                                                                        Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic
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and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, or human polymucleotides or a polymucleotide which represents a fragment, a derivative or allelic variation of the nucleic acid sequence. Also calaimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kief to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polymorleotides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity of one or more of the polympetides or their an animal of one or more of the polympetides or their antibodies. The polymucleotide or the compound that sequence its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at fig. who. int/pub/published_pct_sequences.
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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
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husen BD;
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L, Patturajan M, Shimkets RA, Casman SJ, Malyan P, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook J Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     designated NOVX, useful for treationsity, dyslipidemia, anorexia, immune and hematopoietic disorde
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2000US-0255029P.
2001US-0263800P.
2001US-0269942P.
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24-JAN-2001;
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syndrome associated with a human disease, preferably a NOVX-associated disorder, or for treating or preventing a NOVX associated disorder in a subject, preferably human. The isolated protein, its encoding polymucleotide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorder, Alzheimer's disease, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with chronic diseases, and cancer. The isolated protein are useful for chronic diseases, and cancer. The isolated protein are useful for chronic diseases, and cancer. The isolated protein are useful for creating or preventing neurological disorders such as epilepsy, stroke, mental disorders including mood, anxiety, schizophrenic disorders, diabetes disorders of vesicular transport such as cystic fibrosis, diabetes mellitus, goiter, gastrointestinal disorders including ulcerative colitis, other conditions associated with abnormal vesicle trafficking including ADDS, allergic reactions, multiple sclerosis and rheumatoid arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynucleotide of the invention can be used to treat disorders by gene therapy. This sequence represents one of the isolated NOVX proteins of the invention
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2000US - 0246529P

2000US - 0246521P

2000US - 024921P

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14-SEP-2000;
15-SEP-2000;
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20000US - 0180628P.
20000US - 0184664P.
20000US - 0189874P.
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20000US - 0198123P.
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20000US - 02118290P.
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2000US - 0225266P.
20000US - 02231244P.
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20000US - 02331244P.
20000US - 0233296P.
2000US - 0232399P.
2000US - 0232399P.
2000US - 0232399P.
2000US - 02323460P.
2000US - 0232399P.
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24-FEB-2000;

24-FEB-2000;

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19-MAY-2000;

10-MAR-2000;

10-MAR-2000;

11-JUL-2000;

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                                                                                                                                                            sapiens
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muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
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20000US - 02144886P.
20000US - 0216647P.
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20000US - 0229343P.
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20000US - 022945P.
2000US - 0239497P.
20000US - 02394997P.
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                                                                                                                                                                         -JAN-2001;
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28-JUN-2000;

07-JUL-2000;

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14-AUG-2000;

17-NOV-2000;

17-NOV-2000;

17-NOV-2000;

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17-NOV-2000;

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                                                                                            sapiens
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(RUBE/)
(BARA/)
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y. cardiac
giogenesis,
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rbant as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be 1
                                                                                                                                                                                                                                                              The invention relates to isolated nucleic acids and proteins are used encoded secreted proteins. The nucleic acids and proteins are used brevent, treat or ameliorate a medical condition in e.g. humans, micrabbits, goats, horses, cats, dogs, chickens or sheep. They are also in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant (ELISA). Disorders which are diagnosed or treated include autoimmuno diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cerebral schaemia, angiogen nervous system disorders e.g. Alzheimer's disease, infections cause are disorders e.g. Alzheimer's disease, infections cause bacteria, viruses and fungi and coular disorders e.g. corneal infect and many other disorders e.g. Alzheimer's disease, infections cause to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note sequence data for this patent did not form part of the printed
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                                                                                                                                                                                    New nucleic acid molecules encoding 461 diagnosing, preventing, treating or amelused as food additives or preservatives.
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Pred. No.
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 2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251990P.
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100.0%;
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                                                                                                                                                                                                                                          1141;
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Best Local Similarity 100.
                                                                                              SCI
                                                                                                                       SC,
                                                                                              GENOME
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AAS26175.
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                                                                                                                       Barash
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                                                                                              HUMAN
 08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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11-DEC-2000;
05-JAN-2001;
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                                                                                                                                               WPI; 200
N-PSDB;
                                                                                             (HUMA-)
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i disorder;
le sclerosis;
v disorder;
                             treating,
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irrhosis;
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                                                                                                                        The invention relates to human novel polypeptides and their associa polynucleotides. The polypeptides and polynucleotides are useful in the rapy for treating, inhibiting or preventing neural disorders, important disorders, respiratory disorders, in asal vestibulitis, nasal polyps and sinusitis), reproductive disorders describilitis, nasal polyps and sinusitis), reproductive disorders describilitis, nasal polyps and sinusitis), reproductive disorders describilitis, nasal polyps and sinusitis), reproductive disorders describilitis and disorders describilities and hypoplastic leart syndrome), renal disorders (e.g. acute kidney failure and end renal disease), hyperproliferative disorders (e.g. Hodgkin's disease leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blo related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
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                           therapy for t
m, muscular,
nary, cardiova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system diseaselsener, s disease; Parkinson's disease; epilepsy; multiple so schizophrenia; depression; autoimmune disorder; inflammatory disportasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis colon cancer; lung cancer; liver cancer; brain cancer; melanoma; liver disease; liver cilung disease; emphysema; obstructive pulmonary disease; haemoph:
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                           otides and nucleic acids, useful in gene there or preventing e.g. neural, immune system, mus
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Mismatches 0;
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Pred. No.
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Best Local Similarity 100.0%;
Matches 159; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                  ID NO 1141;
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                             New polypeptides
inhibiting or pre
 ABX73516
                                                                                                                                                                                                                                                                                                                                                                 165 AA;
                                                       espiratory, repenal disorders
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                                                                                                    11; SEQ
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                                                                                                                                                                                                                                                                                                                                                                  Sequence
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N-PSDB;
                                                                                                   Claim
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ABO1464
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The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polynucleotide is useful for treating endocrine/ metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus, asthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of drugs during clinical trials. This is the amino acid sequence of a novel human NOV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
                                                                                                                                                                                                                                                                                                         Li L, Anderson DW, Zhong M;
Berghs C, Rothenberg ME, Guo X;
Kekuda R, Ji W, Miller CE;
Liu X, Padigaru M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOV and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.
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Pred. No. 3.1e-87;
); Mismatches 0;
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Ellerman K,
Catterton E,
Shenoy SG, L
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2001US-0318120P.
2001US-0318130P.
2001US-0318430P.
2001US-0322636P.
2001US-0322816P.
2001US-0322816P.
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larity 100.0%;
Conservative
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Vernet CAM,
A, Leach MD,
Taupier RJ,
Edinger SR,
                                                                                                                                                                                                                                                                                                          Σ
                                                                                                                                                                                                                                                                            CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-313242/30
N-PSDB; ACD19339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 108; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Æ;
 07-SEP-2001;

07-SEP-2001;

10-SEP-2001;

17-SEP-2001;

17-SEP-2001;

17-SEP-2001;

17-SEP-2001;

20-SEP-2001;

20-SEP-2001;

20-SEP-2001;

25-SEP-2001;

26-SEP-2001;

26-SEP-2001;

26-SEP-2001;

26-SEP-2001;

26-SEP-2001;

26-SEP-2001;

26-SEP-2001;
                                                                                                                                                                                                                                                                                                      Spytek KA, F
Gerlach VL,
Shimkets RA,
Rieger DK, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 203
                                                                                                                                                                                                                                                                                                                                                   DK,
                                                                                                                                                                                                                                                                                                                                                                             Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105
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ID AAU1
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standard; protein;

AAU16603

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20000US - 023329BP - 20000US - 023449BP - 20000US - 023449BP - 20000US - 02344617P - 20000US - 02346474P - 20000US - 02346529P - 20000US - 02346652P - 20000US - 023466619P - 20000US - 0246652P - 20000US - 024665
tion;
d additive;
                                                                                                              ';
sorder;
                                                                                                                                   der;
                                                                                Human; immunosuppressive; antiarthritic; antirheumatic; cytost cardiant; vasotropic; cerebroprotective; nootropic; neuroprote antibacterial; virucide; fungicide; opthalmalogical; vulnerary secreted protein; rheumatoid arthritis; hyperproliferative discardiovascular disorder; cardiac arrest; cerebrovascular disorcerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection healing; epithelial cell proliferation; skin ageing; foo preservative; antiproliferative.
                                                             S
                                                                                                                                                                                                                                                                                                   2000US - 0179065P.
2000US - 0184664P.
2000US - 0184664P.
2000US - 0189874P.
2000US - 01998123P.
2000US - 0198123P.
2000US - 0209467P.
2000US - 0214886P.
2000US - 0218290P.
2000US - 0218290P.
2000US - 0225266P.
2000US - 0225268P.
2000US - 0225268P.
2000US - 0225268P.
2000US - 0225275P.
2000US - 0225279P.
2000US - 0225278P.
2000US - 0225278P.
2000US - 0225759P.
2000US - 0225344P.
2000US - 0229344P.
                                                             protein,
                                      entry)
                                                             secreted
                                    (first
                                                                                                                                                                                                                                 WO200155322-A2
                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                    31-JAN-2000;

24-FEB-2000;

02-MAR-2000;

17-MAR-2000;

17-MAY-2000;

19-MAY-2000;

19-MAY-2000;

10-JUL-2000;

11-JUL-2000;

11-JUL-2000;

11-JUL-2000;

14-AUG-2000;

14-AUG-2000;

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15-AUG-2000;

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18-AUG-2000;

18-AUG-2000;

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18-AUG-2000;

18-AUG-2000;

19-AUG-2000;

10-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

06-SEP-2000;

08-SEP-2000;

08-SEP-2000;
                                                           novel
                                    07-NOV-2001
                                                                                                                                                                                                                                                                                -JAN-2001
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              AAU16603
                                                                                                                                                                                                          Homo
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.Oligo

-650-12

10-078

 $\boldsymbol{\omega}$ ₽

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Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                      2000US-0119065P.
2000US-0214886P.
2000US-0216647P.
2000US-0216647P.
2000US-0216647P.
2000US-0217486P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-02217487P.
2000US-0225270P.
2000US-02254519P.
2000US-02254519P.
2000US-02254519P.
2000US-0225451P.
2000US-02254519P.
2000US-02254519P.
2000US-02254519P.
2000US-0225451P.
2000US-0236367P.
2000US-0236367P.
2000US-0236369P.
2000US-0236369P.
2000US-0237039P.
2000US-0237039P.
2000US-0237039P.
2000US-0237039P.
2000US-0237039P.
2000US-0237039P.
2000US-0237039P.
2000US-0234617P.
2000US-0231868P.
2000US-0231868P.
                                 #759
                                                                                                                                                                                                                                                                             2001US-00764864
    entry)
                                polypeptide
   (first
                                                                                                                                                                                                                   US2002132753-A1
                                                                                                                                                                                                                                                                              -JAN-2001;
                                                                                                                                                                                                                                                                                                         31-JAN-2000;

28-JUN-2000;

07-JUL-2000;

07-JUL-2000;

11-JUL-2000;

14-AUG-2000;

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14-AUG-2000;

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14-AUG-2000;

15-JUL-2000;

16-AUG-2000;

17-AUG-2000;

17-AUG-2000;

18-BP-2000;

18-BP-2000;

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19-SEP-2000;

19-SEP-2000;

29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

20-OCT-2000;

20-OCT-2000;
                                                                                                                                                                                      sapiens
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   8-MAR-2003
                                  novel
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                                  Human
                                                                                                                                                                                      Ношо
   , mice,
also used
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to such a wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the printed of the printed sequence. These patent did not form part of the printed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     logenesis,
saused by
infection,
septides
iferation,
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cardiac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGHLEKAVVLELTLKHLKALTALTEQQHQKIJALQNGERSLKSPIQSDLDAFHSGFQTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecules encoding 461 human secreted proteins diagnosing, preventing, treating or ameliorating medical conditused as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Lt
1.8e-86;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 107; DB Pred. No. 1.800; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                      980pp;
                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
2000US-0251030P.
2000US-0251988P.
2000US-0251988P.
2000US-0251868P.
2000US-0251869P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                       1556;
                                                                                                                                                                                                                                                  SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                   GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                       11; SEQ ID NO
                                                                                                                                                                                                                                                                                                               2001-488783/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 107; Conser
                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS26590
  17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                   11-DEC-2000
05-JAN-2001
                                                                                                                                                                                                                                                                                G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44
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D ABU55672
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104
                                                                                                                                                                                                                                                                                  Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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ZЪ C) W

ROSEN RUBEN

(ROSE/) (RUBE/)

ABU55672;

XXXX

RESULT 14

Matches

dd

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loop helix protein of the DEC family for use in for treatment of disorders of cell differentiation

Japanese

B

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DEC2a; DEC2b; bHLH type transcription factor; DEC2; DEC1; basic helix loop helix protein; cell differentiation; prolifer
                                                                                                                                                                                                                                                    LGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFH
                                                                                                                                                                                                                                                                               KEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPL
                                                                                                                                                                                                                        Score 107; DB 6; I
Pred. No. 1.8e-86;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       DEC2a protein sequence SEQ ID NO:14
                                                                                  English
                                                                                 402pp;
              Barash SC;
                                                                                                                                                                                                                   22.1%; SU
100.0%; Pi
0;
                                                                                                                                                                                                                                                                                                                               410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-00233286
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-JP003991
                                                                                                                                                                                                                                                                                                                              AAB70694 standard; protein;
                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                 1556;
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEIYAKU
             Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shin M,
                                                                                  8
                                                                                                                                                                                                                                                                                                                                                          (first
                           WPI; 2003-147444/14
N-PSDB; ABX73931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-202935/20
 U
                                                                                                                                                                                                                               l Similarity
107; Conser
                                               New polypeptides
inhibiting or pre
                                                                                  ΩÏ
                                                                                                                                                                                                            Sequence 150 AA;
                                                            respiratory, reprenal disorders
BARASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHUGAI
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200114551-A1
                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                         musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                          17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쩟
                                                                                 11;
             GA,
                                                                                                                                                                                                                                                                                                                                            AAB70694;
                                                                                                                                                                                                                        Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHUS)
                                                                                                                                                                                                                               Local
(BARA/)
              Rosen
                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                        Mouse
                                                                                                                                                                                                                        Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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#XIXEEXXFFFFFXXXXDDDDDDDDDXXXXX
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Gaps

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Indels

141

SGFOTCA

103

SGFOTCA

188

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The present invention describes a basic helix loop helix (bHLH) type transcription factor designated DEC2. DEC2 can be used as a tool in the development of drugs for the treatment and prevention of disorders involving cell differentiation and proliferation. The present sequence represents the specifically claimed mouse DEC2a protein, as given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 DTYKLPHRLIEKKRRDRINECIAQLKDLLPEHLKLTTLGHLEKAVVLELTLKHLKALTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.7%;
100.0%;
                                                                                                                                                                        83pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: December 15, Job time: 164 secs
                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                DEC2 is a basic helix development of drugs fand proliferation.
                                                                                                                                                                          Claim 2; Page 77-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 81; Conser
                                                                                                                                                                                                                                                                                                                                                                                present invention
 N-PSDB; AAF74777
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human novel polypeptides and their associated polynuclectides. The polypeptides and polynuclectides are useful in gene polynuclectides. The polypeptides and polynuclectides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. system disorders (e.g. respiratory diseases (e.g. and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and multiple sclerosis), muscular disorders, respiratory diseases (e.g. cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABU54914-ABU55699 and ABU55748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                             vascular
                                                                                                                                                                                                ptides and nucleic acids, useful in gene therapy for or preventing e.g. neural, immune system, muscular, y, reproductive, gastrointestinal, pulmonary, cardio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 150;
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102
43 DTYKLPHRLIEKKRRDRINECIAQLKDLLPEHLKLTTLGHLEKAVVLELTLKHLKALTAL
                                                                                                                                                   2004, 20:10:58
                                                    125
                                                  TEQQHQKIIALQNGERSLKSP
||||||||||||||||||
TEQQHQKIIALQNGERSLKSP
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.. 0

Gaps

·. 0

Indels

· 0

Score 81; DB 4; L. Pred. No. 5.3e-63; 0; Mismatches 0;

,

Length 410;

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5.1.6
Compugen Ltd.
 GenCore version (c) 1993 - 2004
           Copyright
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- protein search, using sw model OM protein

; Search time 41 Seconds (without alignments) 1135.827 Million cell updates/sec 2004, 19:36:35 December 15, Run on:

score:

US-10-078-650-12 2517 1 MDEGIPHLQERQLLEHRDFI.....PGNPESSAQEDPSQPGKEA Title: Perfect so Sequence:

P 484

Gapext BLOSUM62 Gapop 10.0 , Scoring table:

283416 segs, 96216763 residues Searched:

0.5

283416 of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* 10 m 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description        | asic helix-loop- | asic helix-loop- | asic helix-loop- | thetical pro | egmentation prot | ranscription fac | ranscription fac | elix-loop-helix | ypothetical prot      | REAC-4 - huma | ypothetical prot      | mmediate-early p | ranscription | TP-binding regul | pidroin 2, dragl | ermal gland prot | ranscription fac | mmediate-early p | ypothetical prot | egument protein | mmediate-early p | ialidase - Actin | -box prote | ypothetical prot | vx1 protein - mu | -chimerin | ypothetical prot | ibroin - Chine | bable multi-d |
|-----------|--------------------|------------------|------------------|------------------|--------------|------------------|------------------|------------------|-----------------|-----------------------|---------------|-----------------------|------------------|--------------|------------------|------------------|------------------|------------------|------------------|------------------|-----------------|------------------|------------------|------------|------------------|------------------|-----------|------------------|----------------|---------------|
| SUMMAKIES | ID                 | <br>C758         | C758             | C554             | T33110       | 2971             | 5302             | 3674             | 4623            | 2234                  | 0273          | 1514                  | DBE2             | 5333         | 5241             | 4411             | KXLA             | 4964             | DBE2             | 2901             | 4256            | DBEX             | 4922             | 0184       | 4628             | 1254             | 0000      | 0036             | 3132           | 5056          |
|           |                    | 9.2              | 10               | 12               |              | 18               | 80               | 81               | 35              | 81                    | 65            | 18                    | 26               | 82           | 46               | 27               | 16               | 20               | 94               | 10               | 34              | 25               | 01               | 02         | 62               | 16               | 03        | 80               | 39             | 34            |
| ø¥.       | Query<br>Match Len | 9.2              | 4.9              | 9.9              | ۳.           | ٠,               | 4.               | ۳.               | ۳.              | ~.                    | ~!            | ~.                    | ۲.               | 0.           | ٥.               | ٥.               | ٥.               | ∞.               | ω.               | ω.               | В               | ω.               | ۰.               | ۲.         | .7               | .7               | .7        | 9.               | .6             | .5            |
|           | Score              | 2498             | 63               | 99               | •            | α                | 18               | •                | 82.             | $\boldsymbol{\omega}$ | Ø             | $\boldsymbol{\omega}$ | •                | ~            | ~                | 75.              | 72.              | 71.              | ٠                | 71.              | 71.             | 70.              | 7                | Ø          | 16               | •                | 67.       | φ                | 16             | •             |
|           | Result<br>No.      | <br>             | 7                | m                | 4            | വ                | v                | 7                | α               | σ                     |               |                       |                  | 13           |                  |                  |                  |                  |                  |                  |                 |                  |                  |            |                  |                  |           |                  |                |               |

|   | hypothetical prote |      | serine-rich protei | prot | mentation p | ranscrip       | rot  | ancer | cription fa | HLF1 protein - h | hosphoprotein, | (2)<br>(2) | asic helix-loo | stin precurs | related to cytoske | hypothetical prote |
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|   |                    | 93   | ~                  | 58   | m           | 4              | ~    | 0     | 0           | 099              | 0              |            | ~              |              | 11                 |                    |
|   | •                  | •    | •                  | •    | •           | •              | •    | •     | •           | 6.3              | •              | •          | •              | •            | •                  | •                  |
|   | •                  | 16   | 62.                | •    | 16          | 61.            | 60.  | ω,    | 59.         | 159              | 7.             | S          | ß              | S            | S                  | 2                  |
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| • |                    |      |                    |      |             |                |      |       |             |                  |                |            |                |              |                    |                    |

## ALIGNMENTS

| RESULT JC7583  Dasic I C, Speci C, Date; C, Acces R, Fujin Biochen A, Refer A, Resic A, Molec C, Genet C, Genet C, Genet A, Map F, 130-1 F, 130-1 | RESULT 1 JC7583  Dasic helix-loop-helix protein, DEC2 - human C;Species: Homo sapiens (man) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004 C;Accession: JC7583 E;Fujimcto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. Biochem: Blophys. Res. Commun. 280, 164-171, 2001 A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-loo A;Reference number: JC7583; MUID:21092582; PMID:11162494 A;Accession: JC7583 A;Molecule type: mRNA A;Residues: 1-482 <fuj> A;Residues: 1-482 <fuj> A;Residues: 1-282 <fuj> A;Residues: 1-22-212.1 C;Genetics: A;Gene: dec2 A;Genetics: A;Genetics: A;Gene: dec2 A;Genetics: A;Genetics: A;Gene: dec2 A;Genetics: A;Genetics:</fuj></fuj></fuj> |
|---|---|
| Query   | ery Match   |
| Best  | st Local Similarity 99.6%; Pred. No. 4.8e-140;  |
| Match   | cches 482; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  |
| Qy  | 1 MDEGIPHLQERQLLEHRDFIGLDÝSSLYMCKPKRSMKRDDTKVSDTYKLPHRLIEKKRRD 60   |
| Db  |   |
| Qy  | 61 RINECIAQLKDLLPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGER 120   |
| Dp  |   |
| oy  | 121 SLKSPIQSDLDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQ 180  |
| Oy  |   |
| ζζ,   | 181 LLTQQVPLSKGTGAPSAAGSAAAPCLERAGQKLEPLAYCVPVIQRTQPSAELAAENDTDT 240  |
| GD  |   |
| 95  | 241 DSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDSPAPKRMKLDSRGGGSGGGPGGGAA 300  |
| DP  |   |
| & g   | 301 AAAALLGPDPAAAALLRPDAALLSSLVAFGGGGAPFPQPAAAAPFCLPFCFLSPSA 360<br>  |
| δλ  | 361 AAAYVQPFLDKSGLEKYLYPAAAAPFPLLYPGIPAPAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   |

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Dasic helix-loop-helix factor DEC1 - human cispecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5547
C;Accession: JC5547
B;Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.; Rishen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.; Biochem. Biophys. Res. Commun. 236, 294-298, 1997
A;Title: Molecular characterization of the novel basic helix-loop-helix protein DEC1 exp. A;Reference number: JC5547
A;Molecule type: mRNA
A;Residues: 1-412 <SHE>
A;Residues: 1-412 <SHE>
A;Residues: 1-412 <SHE>
A;Cross-references: UNIPROT:O14503; DDBJ:AB004066; NID:g2308996; PIDN:BAA21720.1; PID:g2:C,Comment: This protein is involved in the control of cell differentiation in several tife;51-108/Region: helix-loop-helix #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C18H7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33110
R;Tin-Wollam, A.; Fronick, W.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C18H7.
A;Reference number: Z21284
A;Reference number: Z21284
A;Reference number: Z21284
A;Reference number: Z1284
A;Reference specimental source: Strain Bristol N2; clone C18H7
A;Experimental source: strain Bristol N2; clone C18H7
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Matches 191; Conservative 55
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JC7584
basic helix-loop-helix protein, DEC2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Accession: JC7584
R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.
Biochem. Biophys. Res. Commun. 280, 164-171, 2001
A;Title: Molecular cloning and characterization of DEC2, a new m A;Reference number: JC7583; MUID:21092582; PMID:11162494
A;Accession: JC7584
A;Accession: JC7584
A;Accession: JC7584
A;Cross-references: UNIPROT:099PV5; DDBJ:AB044090
C;Comment: This protein, a novel member of the DEC subfamily of C;Genetics:
A;Gene: dec2
A;Map position: 6 G2-G3
C;Keywords: transcription factor
F;1-173/Region: highly conserved #status predicted
F;11-173/Region: alanine and glycine-rich #status predicted
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Pred. No. 3.2e-89;
21; Mismatches 37;
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Best Local S
Matches 86
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                                                                                                                     GAPSAAGS - - - AAAPCLERAGOKLEPLAYCVPVIORTOPSAELAAENDTDTDS
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                                                                                                                                             --GPAGPPGPPGPNGEAGAGS
                                                                                                                                                                                           --GADGAPGTDAA
                                                                                                                                                                                                                  -AAAAALLGPDPAAA---AALLRPDAALLSSLVAFGGGGGAPFPQPAAAAPF
                                                                                                                                                                                                                                                                                                                                        -GGGAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 LIEKKRRDRINECIAQLKDLLPEHLKLTTLGH--LEKAVVLELTLKHLKALTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SAAGSAAAPCLERAGO
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                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
S29712
segmentation protein hairy - red flour beetle
C; Species: Tribolium castaneum (red flour beetle)
C; Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_cha
C; Accession: S29712
R; Sommer, R.J.; Tautz, D.
Nature 361, 448-450, 1993
A; Title: Involvement of an orthologue of the Drosophila pair
A; Reference number: S29712; MUID: 93156810; PMID: 8429884
A; Accession: S29712
A; Accession: S29712
A; Molecule type: DNA
A; Molecule type: UNA
A; Cross-references: UNIPROT: Q8T306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLNÓGQKEPQVQVIVPEVAPNNILLGNGTGVQLVPIRLANGDIA-
                                               protein
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                                                            Score 209.5; DB 2;
Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 188; DB 2;
Pred. No. 0.00024;
28; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LLTQQVPLSKGTGAP---
                                                                                                                                                                                                                                                                                                                                       -PDAAAAAPEAAABEAAPAAEGA-
                                               wall
                                                                                                                                                                                           ---PGKDGDA
                                              glycine-rich cell
                                                                                                                                            186 GKPGAAGSDGEAGAPGTKTTNAPGEP-
                                                                                             15;
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ilarity 30.1%;
Conservative 20
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                                                                              Similarity 31.999; Conservative
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                                               Phaseolus
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Best Local Similarity
Matches 72; Conser
C;Genetics:
A;Gene: CESP:C18H7..
A;Map position: 4
A;Introns: 84/1
C;Superfamily: Phase
                                                                     Query Match
Best Local S
Matches 99
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S36748
transcription factor HES-1 - rat
N;Alternate names: hairy-like gene RHL; helix-loop-helix protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Dec-1933 #sequence_revision 10-Nov-1995 #text_change 09-J
C;Accession: S36748; A48106
R;Sasai, Y; Kageyama, R.; Tagawa, Y.; Shigemoto, R.; Nakanishi, S.
Genes Dev. 6, 2620-2634, 1992
A;Title: Two mammalian helix-loop-helix factors structurally related
A;Reference number: S36748; MUID:94040724; PMID:1340473
A;Reference number: S36748; MUID:94040724; PMID:1340473
A;Residues: 1-281 <SAS>
A;Cross-references: UNIPROT:Q04666; EMBL:D13417; NID:g220760; PIDN:B
R;Feder, J.N.; Jan, L.Y.; Jan, Y.N.
Mol. Cell: Biol. 13, 105-113, 1993
A;Title: A rat gene with sequence homology to the Drosophila gene ha
A;Reference number: A48106
A;Reference number: A48106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85,'N',94-281 <FED>
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                                                                                                       change
                                                                                                                                                                                                  HRY,
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transcription factor HES-1 - human
N;Alternate names: hairy protein homolog
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_cha
C;Accession: A53027
R;Feder, J.N.; Li, L.; Jan, L.Y.; Jan, Y.N.
Genomics 20, 56-61, 1994
A;Title: Genomic cloning and chromosomal localization of HRY
A;Reference number: A53027; MUID:94292187; PMID:8020957
A;Accession: A53027
A;Accession: A53027
A;Accession: A53027
A;Accession: A53027
A;Cross-references: UNIPROT:Q14469; GB:L19314; NID:g436999;
C;Genetics:
A;Gene: GDB:HRY
A;Cross-references: GDB:217077; OMIM:139605
A;Map position: 3q28-3q29
C;Keywords: immediate-early protein
                                                                                                                                                                                                                                                                                                                                             GB:L19314; NID:g436999;
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Local Similarity 27.5%;
les 86; Conservative 2
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79 DILEMTVKHLRNL---
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EMBL: Z77662; PIDN: CAB01192.1; GSPDB: GN00023;
                       351
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                                                                                                                                              - ENLIHTLPGQTQLPVKNSTSPPLSPISSISSHCEESR
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                                                                                                                  SRGGGSGGGPGGGAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAA
                                                                 KPVNTSVPANL
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C; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_cl
C; Accession: G02738
R; Enerback, S.
submitted to the EMBL Data Library, June 1996
A; Reference number: H01646
A; Accession: G02738
A; Accession: G02738
A; Accession: G02738
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-465 < ENEA
A; Cross-references: UNIPROT:Q16676; EMBL:U59832; NID:g13992
C; Genetics:
A; Conetics:

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                                                  -GTASAALASIANPTHLNDYTQSFRMSAFS
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Pred. No. 0.0016;
; Mismatches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122/3; 148/3; 194/1;
                                                                                                                                                                                                             PPPEKA
                                                                                                                                                                                                                                                          AASPTV-DVLSKHSFAGVFSTPPPTSA
                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F47B8.5 - Caenorhabd C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15 C; Accession: T22341
R; Berks, M.; McMurray, A. submitted to the EMBL Data Library, July A; Reference number: 219551
A; Accession: T22341
A; Accession: T22341
A; Accession: T22341
A; Accession: T22341
A; Experiment al source: clone F47B8
C; Genetics: A; Experimental source: clone F47B8
C; Genetics: A; Genetics: A; Hay Position: 5
A; Map position: 5
A; Introns: 37/3; 82/3; 122/3; 148/3; 194/
                       GGGAAAAAALLGPDPAAAAALLRP
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Best Local Similarity 31.9%;
Matches 72; Conservative
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                                                                                                                                                                                         -LEKA
                                                                                                                                                                                                                                                                                                                                  -STDPSVLGKYRAGFSECMNEVTRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSAPCKLGSQAGEAAKVFGGFQVVPAPDGQFA
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                                                                                                                                                                                                                                                                                                                                                                                  SAAGSA
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 ; PID:9204
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                                                                                                                                                                                       KPKRSMKRDDTKVSDTYKLPHRLIEKKRRDRINECIAQLKDLLPEHLKLTTLGH
                                                                                                                                                                                                                                                                                                                                                                                  --LPTPQLLTQQVPLSKGTGAP
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                                                                                                                                                                                                                  ---SEHRKSSKPIMEKRRRARIŅESLSQLKTLILDALKKDSSRH
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A46231
helix-loop-helix protein Dpn - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 1
C;Accession: A46231
R;Bier, E.; Vaessin, H.; Younger-Shepherd, S.; Jan, L.Y.; Jan, Y.
Genes Dev. 6, 2137-2151, 1992
A;Title: deadpan, an essential pan-neural gene in Drosophila, enc
A;Reference number: A46231; MUID:93051333; PMID:1427077
A;Accession: A46231
A;Accession: A46231
A;Accession: A46231
A;Cross-references: GB:S48025; NID:g259771; PID:g259772
A;Note: sequence extracted from NCBI backbone (NCBIN:117859, NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      change
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                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASRVTIKQEPPGEDSPAPKRMKLDSRGGGSGGGGGGAAAAALLG-
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A; Cross-references: GB:L04527; NID:g204554; PIDN:AAA41307.1 A; Note: sequence extracted from NCBI backbone (NCBIN:121122 C; Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LIMPNTĠSAAPP
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--SAPAIQMGGLQLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 7.3%; Score 182.5; DB 2; Similarity 21.7%; Pred. No. 0.0011; 97; Conservative 53; Mismatches 146;
                                                                                           Score 183.5; DB 2;
Pred. No. 0.00058;
25; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -WTPREPRCVQLINHL
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                                                                                                                                                                                                                                                                                                                                                                                  SRFESWIPREPRCVQLINHLHAVATQF--
                                                                                                                                                                                                                                                                                                                               DILEMTVKHLRNL-----QRAQMTAAL
                                                                                                                                         25;
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                                                                                            th 7.3%;
Similarity 27.0%;
84; Conservative 2
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Matches 84
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CESP: F4'

| arly protein IER2.9 - names: early protein bovine herpesvirus 1 Dec-1992 #sequence_rev: B38209 V.; Fraefel, C.; Vogt, C. 2763-2772, 1992 mediate-early RNA 2.9 number: A38209; MUID: B38209 type: DNA 1-676 <wir> erences: UNIPROT: P2912 ly: herpesvirus immediat in: RING finger homolc ion: zinc finger C3HC4 egion: acidic</wir> | Query Match 7.1%; Score 179.5; DB 1; Length 676; Best Local Similarity 28.5%; Pred. No. 0.0026; Matches 92; Conservative 35; Mismatches 125; Indels 71; Gaps 15; | 0y 171 WITCPLETFOLLTQCVPLEXGTGAPSAAGSAACARACLERA-GCKLEPLAN-UPVIRETOPS 229  Db 352 VGTRRGTEAN-OPARGIARRPCGRAAANSAPBSSRSGGRDBRLPAARARA 406  Oy 230 ARLAARNDIDDDSGYGGB-AERAPDZEXGGGAGARRYIKGEPGEDSPARKR 281  Db 407 AQARCGSPERREAGCLCVAAGTAGWGAGSESGRERRALLGEGPRVQARRRR 466  OY 282 WILDSRGGGSGGGGGGGGAAAAAAALGPPAALLSSLVAFGGGGGPRVQARRRR 466  OY 282 WILDSRGGGSGGGGGGGGAAAAAAALGPPAALLGPPAALLSSLVAFGGGGGP-FF 7339  Db 467 TELDR  |
|--|--|--|
| Query Match   7.2%;   Score 181;   DB 2;   Length 465;     Best Local Similarity   29.5%;   Pred. No. 0.0014;     Matches   100;   Conservative   21;   Mismatches   104;   Indels   114;   Gaps   19;     OY   235 ENDTDTDSGYGGEABARPDREKGKGAGASRVTIKQE   | Oy 436 LPHEVAPLGAPHPQHPHGRTHLPFAGPREPGNPESSA 472<br>:  | RESULT 11  T15142  T15 |

| 7.0%; Score 177; DB 2  |   |
|--|---|
| Best Local Similarity 26.7%; Pred. No. 0.0014; Matches 83; Conservative 25; Mismatches 95; Indels 108; G   | QY 313 AAAALLRPDAALLSSLVAFGGGGAPFPQPAAAAAPFCLPFCFLSPSAAAAYVQPFL 369   |
|  | 370 DKSGLEKYLYPAAAAPFPLLYPGIPAPAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  |
| LELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTCA  | DD 286VWGARSLSATPAARASLPARAAAARAASAARAVAAGRSASAAPSRAHLRPP 337   |
| DD 79 DILEMTVKHLRNLQRAQMTAALSTDPSVLGKYRAGFSECMNEVTRFL 125  | Qy 424 PPEKAGAAATLLPHEVAPLGAPHPQHPHGRTHLPFAGPREPGNPESSAQEDPSQ 478   |
| Qy 149 SRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSA 201   | DD 338 SPEIQVADPPTPRPAPRPSAWPDKYERGRSCCRYEAASGICEIESSSDESE 388 Qy 479 PG 480  |
| 202 AAPCLERAGQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKGKGAG 26<br>  | 389   |
| 184 PPPPPLVPIVPI   | 15  |
| GEAAKVFGGFQVVPAPDGQFA 23   | oin 2, dragline<br>ernate names: s  |
| 317 LLRPDAALLSS 3  | : 31-Dec-1993 #seque<br>ssion: A44112; S2782  |
| 45 CLATRONGALMS 24   | ol. Chem. 267, 19320<br>le: Isolation of a c  |
| SULT 12418   | erence number: A44112; MUID:92406876; PMID:1527052  |
| P-binding regulatory protein Gs alpha-Alternate names: G protein XL-alpha-s  | cus: preliminar   |
| species: kattus norveg<br>Jate: 14-Jul-1995 #seq<br>Accession: S52418  | ldues: I-02/ Aniny<br>ss-references: UNI<br>s: sequence extrac  |
| Kehlenbach, R.H.; M. ure 372. 804-809.   | nan, M.B.; Lewis, R.V.<br>:ted to the BMBL Data Library, May 1992   |
| ritle: XL-alpha-s is a Reference number: S524  | ription: Isolation of<br>brence number: S27824  |
| Accession: S52418<br>Molecule type: mRNA   | ession: S27824<br>ecule type: mRNA  |
| residues: I-<br>Cross-refere<br>Kehlenbach,  | ludes: 19-02/ Chiz.   |
| 375, 253, 1995<br>: Correction: XLalphas is a new typ  | Query Match<br>Best Local Similarity 25.9%; Pred. No. 0.0041;<br>Matches 109: Conservative 20: Mismatches 135: Indels 157; Gaps 18; |
| vererence number: Sport<br>Contents: annotation; assignment of start_codon<br>Note: experimental data from this paper suggest that the translation   | 184 QQVPLSKGTGAPSAAGSAAAPCLERAGQKLEPLAYCVPVIQRTQPSAELAAFNDTDTD 241  |
| Keywords: GTP binding, nucleotide binding; P-loop, signal transduction<br>132-846/Product: GTP-binding regulatory protein Gs alpha-XL chain #status experimenta<br>199-506/Badion: nucleotide-binding motif & (P-loop) |   |
| 744-747/Region: GTP-binding NKXD motif   | 242 SGYGGBAEARPDREKGKGAG-ASRVTIKQEPPGEDSPAPKRMK   |
| Query Match  7.0%; Score 176; DB 2; Length 846;  Best Local Similarity 25.1%; Pred. No. 0.0054;  Matches 106; Conservative 37; Mismatches 133; Indels 146; Gaps 17;  | Db 129 GGYGPGQQGPGGYGPGQQGPGGYGPGQQGPSGPGSAAAAAAAAAGFGQQGPGGYGPGQQG 188<br>Qy 284 LDSRGGGSGGGPGGGAAAAAALLGPDPAAA 314                |
| 105 TEOQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTCAKEVLQYLSRFESW 154   | 189 PGGYGPGQQGPS  |
| DD 69 TTAEBAKVPSLERGEGSPTQPETVHIKPAPVAESGTDSSKADPDSATHAVLQI 121  | OY 315 AALLRPDAALLSSLVAFGGGGAPFPQPAAAAPFCLPFCFL 356   |
| 155 TPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPS   | 22 c  |
| 122 GPEEVGGV   |   |
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     The present invention describes a basic helix loop helix (bHLH) type transcription factor designated DEC2. DEC2 can be used as a tool in the development of drugs for the treatment and prevention of disorders involving cell differentiation and proliferation. The present sequence represents the specifically claimed human DEC2a protein, as given in the present invention
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N-PSDB; ABS76400
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10-AUG-2001;
19-SEP-2001;
26-SEP-2001;
26-SEP-2001;
26-SEP-2001;
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RE,
19-SEP-2002
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Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis, lung disease; emphysema; obstructive pulmonary disease; haemophilia; stroke; infection.
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2001US-0322781P.
2001US-0322816P.
2001US-0323819P.
2001US-0323631P.
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The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polymucleotide is useful for treating endocrine/ metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus, asthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (emphysema or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of-drugs during clinical trials. This is the amino acid sequence of a novel human NOV protein
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 Guo X
 s C, Rothenberg ME, Guo X
a R, Ji W, Miller CE;
Padigaru M, Alsobrook JP;
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                                                                                                                                        New cytoplasmic, nuclear membrane bound or secreted polypeptides (NO' and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia stroke or infections.
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Liu X, Pad
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Pred. No. 5.1e
0; Mismatches
Ellerman K,
Catterton E,
Shenoy SG, I
Burgess CE;
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ilarity 99.6%;
Conservative
CAM,
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RJ,
SR,
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Leach
Taupier
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N-PSDB; ACD19338.
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482; Conser
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Gerlach VL,
Shimkets RA,
Rieger DK, T
Lepley DM, E
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                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
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Pred. No. 5.1e-186;
); Mismatches 0;
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                                                                                                                         gene therapy; vaccine;
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                                                                                                         ovarian
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30-MAY-2002; 2002US-0384531P
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Weng G;
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Alzheimer's dise;
disorder; wound;
                                          New polynucleotide and polypeptide useful for diagnosing, prev
treating conditions such as neurodegenerative diseases, anemia
disorders, wounds, burns, ulcers, osteoporosis, autoimmune discancer.
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                                                                                                                                                                                                                                                                                                       mapping;
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Wang 2
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Y, Asundi
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Wang D, Ma
Drmanac RT;
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N-PSDB; ADC30675.
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and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC3381). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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The invention relates to an isolated polypeptide, designated NOVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polymuclectide or an antibody created from the protein is useful in the manufacture of a medicament for treating a protein, its encoding polymuclectide or an antibody created from the protein are also useful in the manufacture of a medicament for treating a subject, preferably human. The isolated protein, its encoding polymuclectide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, ancreavia, neurodegenerative disorder, Alzheimer's disorders, and various dyslipidaemias, metabolic disturbances associated disorders, and various dyslipidaemias, westing disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with obesity, cherefully neurological disorders such as epilepsy, stroke, mental disorders including mood, anxiety, schizophrenic disorders, and soluters including mood, anxiety, schizophrenic disorders, mellitus, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid architis, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid architis, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid architis, other conditions associated by the polynucleotide of the invention can be used to treat disorders by gene therapy. This sequence invention be used to treat disorders by gene therapy.
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                                                                                                                                                                                        L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM;

[, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP;

Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog Fi

Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;
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                                                                                                                                                                                                                                                                                                                                        designated NOVX, useful for treating of obesity, dyslipidemia, anorexia, and immune and hematopoietic disorders.
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Pred. No. 9.3e-186
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preventing cancer, diabetes, c
metabolic, neurodegenerative,
  2000US-0255029P.
2001US-026326P.
2001US-0263800P.
2001US-0269942P.
2001US-0286183P.
2001US-0313627P.
2001US-0318712P.
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N-PSDB; ABT05457.
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12-DEC-2000;
08-JAN-2001;
24-JAN-2001;
20-FEB-2001;
24-APR-2001;
20-AUG-2001;
12-SEP-2001;
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Tchernev VT
Edinger S,
Colman SD,
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DSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDSPAPKRMKLDSRGGGGGGGGGAA

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2000US-0251660P

06-DEC-2000;

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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment,
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                                                          TDSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDSPAPKRMKLDSRGGGSGGGPGGA
                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                               Rat; pain; neuronal tissue; gene therapy; spinal segmental r
chronic constriction injury; CCI; spared nerve injury; SNI;
                                                                                                 Costigan
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                                                                                                                                                                                                                                                                      ADE54660 standard; protein; 410
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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BAYER AG.
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GENBANK; 035779.
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                                                                                                                                                                                                                                                                                                                                                                                     family for use in cell differentiation
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                                                               PCLSSV
                       Gaps
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                                                       AAAYVQPFLDKSGLEKYLYPAAAAPFPLLYPGIPAPAAAAAAAAAAA
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Pred. No. 9.3e-119;
1; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                     loop helix protein of the for treatment of disorders
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basic helix loop helix protein; cell o
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Best Local Similarity 72.0%;
Matches 350; Conservative
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N-PSDB; AAF74777.
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                                                                                                                  KEAP
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derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the segmental nerve injury (Gung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. spin the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequence.
               858888888888888888888888888888888888
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410 AA; Sequence

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  410;
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                   Indels
 Length
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Pred. No. 5.6e-118;
; Mismatches 37;
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standard; protein;

AB014646

RESULT 12
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Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis; lung disease; emphysema; obstructive pulmonary disease; haemophilia; stroke; infection.
                                                                                                                                                                                                                                                     2001US-0318120P.
2001US-0318130P.
2001US-0322636P.
2001US-0322781P.
2001US-0322816P.
2001US-0322816P.
2001US-0323816P.
2001US-0323813P.
2001US-0323631P.
2001US-0323636P.
2001US-0324969P.
2001US-03249990P.
2001US-03249900P.
2001US-03249900P.
2002US-0373212P.
2002US-0373212P.
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                                       Novel human protein #19
                                                                                                                                                                                           WO2003023002-A2
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07-SEP-2001;
10-SEP-2001;
17-SEP-2001;
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17-SEP-2001;
17-SEP-2001;
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                   25-AUG-2003
ABO14646;
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× Li L, Anderson DW, Zhong M;
Berghs C, Rothenberg ME, Guo X
Kekuda R, Ji W, Miller CE;
Liu X, Padigaru M, Alsobrook JP; l, Gorman L, Ellerman K, Catterton E, Shenoy SG, L Burgess CE; Patturajan M, Vernet CAM, , Leach MD, C CAM, MD, RJ, SR, Taupier Edinger Spytek KA, P Gerlach VL, Shimkets RA, Rieger DK, T Lepley DM, E

WPI; 2003-313242/30 N-PSDB; ACD19339.

New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.

Claim 1; Page 126; 586pp; English.

The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polynucleotide is useful for treating endocrine/ metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus, asthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver

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20000US - 02219290P

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20000US - 0225264P

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20000US - 0225264P

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20000US - 0231244P

20000US - 0225269P

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2000US - 0231244P

20000US - 0231249P

20000US - 0231414P

20000US - 023144P

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         d;
      cirrhosis), lung diseases (emphysema or obstructive pulmonary dinaemophilia, stroke, or infections (e.g. viral, bacterial or parthese are also useful in developing powerful assay system for franalysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of drugs during clitrials. This is the amino acid sequence of a novel human NOV pro
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2.5e-62;
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2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
2000US-0209467P.
2000US-0214886P.
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2000US-0214886P.
2000US-0215135P.
2000US-0215135P.
2000US-0216647P.
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ilarity 88.2%;
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179; Conser
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24-FEB-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
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07-JUL-2000;
11-JUL-2000;
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. recoplasms of the breast or liver, cardiovascular disorders e.g.
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2000US-0246475P.
2000US-0246475P.
2000US-0246476P.
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2000US-0246477P.
2000US-0246477P.
2000US-02466478P.
2000US-0246623P.
2000US-0246523P.
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2000US-0246523P.
2000US-0249209P.
2000US-0249211P.
2000US-0249211P.
2000US-0249211P.
2000US-0249213P.
2000US-0249213P.
2000US-0249213P.
2000US-0249211P.
2000US-0249300P.
2000US-0251988P.
2000US-0251988P.
2000US-0251868P.
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N-PSDB; AAS26175.
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arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
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2000US-0220964P.
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Pred. No. 5.5e-57;
Mismatches (
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2000US-0229343P.
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2000US-0229343P.
2000US-0229344P.
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2000US-023423P.
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2000US-0237039P.
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Similarity 98.8%;
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N-PSDB; ABX73516.
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14-AUG-2000;

22-AUG-2000;

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01-SEP-2000;

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05-SEP-2000;

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29-SEP-2000;

20-OCT-2000;

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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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461 human secreted proteins for ameliorating medical conditions English New nucleic acid molecules encoding 461 diagnosing, preventing, treating or ame used as food additives or preservatives 980pp; Ruben SM; 2000US-0249208P.
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and

The invention relates to isolated nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosassays e.g. radioimmunosassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrals and fungi and coular disorders e.g. corneal infection, bacteria, viruses and fungi and coular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell to protein, carbohydrate, virumins, capabilities, fat content, lipid, protein, carbohydrate, virumins, minerals, cofactors and other nutritional components. The printed sequence data for this patent did not form part of the printed

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Acc72416 Human ova
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Acd19338 cDNA enco
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## ALIGNMENTS

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                                                                                                    transcription factor; DEC2; DEC1;
protein; cell differentiation; proliferation;
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/*tag= a
/product= "DEC2b"
/note= "bHLH type transcription factor"
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                                                                                 sequence SEQ ID NO:11
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                     BP
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                   AAF74776 standard; cDNA; 1511
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WPI; 2003-371981/35 P-PSDB; ADC31646.

renting c s, plate seases or New polynucleotide and polypeptide useful for diagnosing, prevtreating conditions such as neurodegenerative diseases, anemia disorders, wounds, burns, ulcers, osteoporosis, autoimmune dis

1185pp; English 757; ID NO SEQ ;; ; Claim The invention relates to 971 novel human CDNA sequences (ADC29919-CC ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a mucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention dentifying a compound which binds to a polypeptide of the invention. The invention and invention and invention in methods of the invention in methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the polymucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention of ADC33627) and the polypeptides encoded by the contigs (ADC33628 ADC3361). The nucleic acids and polypeptides of the invention are traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or conting and other recombinant production of a protein. The polypeptides and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the printed specification, but was are also obtained in electronic format directly from WIPO at the polypeptides.

831 T; 0 U; 0 Other; ö C; 851 902 Ä BP; 937 3521 Sequence

ö 436 56 67 ហ rtaargaa |||||||| rtaargaa GAAATCG GGGACAT CCCCTTA ||||||| Length 3521; ö CTGGAGAAAGCTGTAGTCTTGGAATTAACTTTGAAACACTTAAAAGCTTTAAC **ACCGAGCAACAGCATCAGAAGATAATTGCTTTACAGAATGGGGAGCGATCTC** ACCGAGCAACAGCATCAGAAGATAATTGCTTTACAGAATGGGGAGCGATCTC Indels ; 0 DB 10; ô Mismatches Score 1378; Pred. No. ( ·. 91.2%; 100.0%; Conservative Best Local Similarity
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The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or parkinson's disease), brain comparing nseful S Kovatis S ), Mills Assessing whether a patient is afflicted with ovarian cancer, assessing the stage or progression of the disease, comprises of the expression level of a cancer marker in a sample from a pat from a non cancer patient. Kamatkar S, Ko n A, Vieby PO, Glatt K; JE, Gannavarapu M, Hoersch S, Kamat E, Morrisey MP, Olandt PJ, Sen A, Lu K, Schmandt RE, Zhao X, Glatt Disclosure; Page 186-187; 481pp; English.

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ic heart also be d with determining

disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determ

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                                                              whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic sequence encodes one of the ovarian cancer markers described in the invention
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R, Ji W, Miller CE;
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Berghs
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2001US-0318130P.
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Shimkets RA,
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The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polynucleotide is useful for treating endocrine/ metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune asthma, inflammatory bowel disease, rheumatoid atthritis or astociaming casthma, inflammatory bowel disease, rheumatoid atthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, osteoarthritis), lung diseases (e.g. colon, lung, liver, breast, ovarian, cirrhosis), lung diseases (e.g. colon, lung, liver diseases (e.g. liver cirrhosis), lung diseases (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of drugs during clinical trials. This sequence encodes a novel human NOV protein
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                                                                                                                                                New cytoplasmic, nuclear membrane bound or secreted polypeptides (NO) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.
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KW CY
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anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes; metabolic disorder; obesity; infectious disease; Alzheimer's disease; anorexia; neurodegenerative disorder; Parkinson's disorder; obesity; immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease metabolic syndrome X; wasting disorder; cancer; neurological disorder; epilepsy; stroke; mental disorder; schizophrenic disorders; goiter; vesicular transport; cystic fibrosis; gastrointestinal disorder; diabetes mellitus; ulcerative colitis; AIDS; allergic reaction; multiple sclerosis; rheumatoid arthritis; transgenic, animal; gene; ds.
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2000US-0255029P.
2001US-0263800P.
2001US-0263800P.
2001US-0269942P.
2001US-0286183P.
2001US-0313627P.
2001US-0318712P.
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12-DEC-2000;
08-JAN-2001;
24-JAN-2001;
20-FEB-2001;
24-APR-2001;
20-AUG-2001;
12-SEP-2001;
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Patturajan M, Shimkets RA, Casman SJ, Malyankar UM; Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP; eyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog isen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD Peyman Eisen A Li L, Ţ, Tchernev VT Edinger S, Colman SD, ×

CURAGEN CORP

(CURA-)

WPI; 2002-547774/58 P-PSDB; ABJ04644.

9 designated NOVX, useful for treating of obesity, dyslipidemia, anorexia, and e, immune and hematopoietic disorders. Novel isolated polypeptide, de preventing cancer, diabetes, metabolic, neurodegenerative,

English 421pp; 43-44; Page <u>ი</u> Claim

The invention relates to an isolated polypeptide, designated NOVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polynucleotide or an antibody created from the protein, its encoding polynucleotide or an antibody created from the protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NoVX-associated disorder, or for treating or preventing a NOVX-associated disorder, or for treating or preventing metabolic disorders, diabetes, obssity, infectious disease, anorexia, neurodespenerative disorders, also useful for infectious disease, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with chronic diseases, and cancer. The isolated protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, with obesity, the metabolic syndrome X, wasting disorders associated with cholynucleotide or an antibody created from the protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, mental disorders including mood, anxiety, schizophrenic disorders, disorders of vesicular transport such as cystic fibrosis, diabetes mental disorders allergic reactions, multiple solerosis and rheumacoid arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynucleotide of the invention can be used to treat disorders by gene therapy. This invention of the invention of the invention of the isolated work. ated with invention the of Se NOVX proteins

Other; 0 ů; 0 •-Н 63  $^{\circ}$ . G 689 784 468 Sequence

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The present invention relates to a microarray comprising a matrix of at least one cDNA probe from a set of probes immobilised to a solid surface in a predetermined order, where a row of pixels corresponds to replicates of one distinct probe from the set. The probes are complementary to nucleic acid sequences that are expressed differentially in aggressive as compared to non-aggressive types of clear cell renal carcinoma (CC-RCC) and that hybridise to the probes under high stringency conditions. The microarray is useful for the prognosis of patients with CC-RCC, wherein aggressive and non-aggressive CC-RCC tumour types are characterised by differential expression profiles of genes that hybridise with one or more probes immobilised on the microarray. The arrays are useful for gene expression profiling of tumour and normal tissues. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New microarray, comprising a matrix of cDNA probe from a set of probes immobilized to a solid surface in predetermined order, useful in the prognosis of patients with clear cell renal carcinoma.
                                                         Human; microarray; solid surface; immobilised probe; CC-RCC; differential expression profile; aggressive CC-RCC tumour type; non-aggressive CC-RCC tumour type; clear cell renal carcinoma; gene expression profiling; tumour tissue; gene; ss.
                                                                                                                                                                                                                                                                      #11 up-regulated in CC-RCC patients.
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervent system disorders e.g. cerebral ischaemia, angiogenesis, nervent system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The printed sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
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                         New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
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2000US-0119065P.
2000US-01180628P.
2000US-0214886P.
2000US-0216647P.
2000US-0217487P.
2000US-0217486P.
2000US-0217486P.
2000US-0217487P.
2000US-0217487P.
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2000US-0229344P.
2000US-0229348P.
2000US-0234997P.
2000US-0234997P.
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2000US-02363636P.
2000US-02363636P.
2000US-0236369P.
2000US-02349299P.
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2000US-0251868P.
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                                                                          polynucleotide
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28-JUN-2000;

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15-EP-2000;

16-JUL-2000;

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11-AUG-2000;

11-
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                                                                          novel
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               ABX7351
                                                                          Human
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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and multiple sclerosis), muscular disorders, cardiovascular disorders, cardiovascular disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent human novel polynucleotides of the invention
                                                                                                                                                           New polypeptides and nucleic acids, useful in gene therapy for treating inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGCAATACCTCTCCCGGTTTGAGAGCTGGACACCCAGGGAGCCGCGGTGTGTCCAGCTGTTCAGCTGTTCAGCTGTTCAGCTGTTTGAGAGCTGGACACCCAGGGAGCCGCGGGTGTGTCCAGCTGTTTGAGAGCTGGACACCCAGGGAGCCGCGGGTGTGTCCAGCTG
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Pred. No. 6.4e-208;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 476; Conservative (
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P-PSDB; ABU55256.
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              ROSEN C A.
RUBEN S M.
BARASH S C
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                                                                                                           disorder
                                                                                                      Human; gene; ds; neural disorder; immune system disorder; renal disorder muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiateriosclerotic.
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Gaps

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193

80

140

253

260

433

320

380

553

440

609

496

12

RESULT

493

373

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2000US - 02312444P

2000US - 02314143P

2000US - 023294144P

2000US - 023298P

2000US - 0232398P

2000US - 023499P

2000US - 024652P

2000US - 024653P

2000US - 024921P

2000US - 024921P
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08-SEP-2000;

08-SEP-2000;

08-SEP-2000;

12-SEP-2000;

14-SEP-2000;

15-SEP-2000;

17-SEP-2000;

18-SEP-2000;

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19-SEP-2000;

11-SEP-2000;

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17-NOV-2000;
17-NOV-2000;
        ion;
additive;
                                                                                                                                                          Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additiv preservative; antiproliferative.
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                                                                                                                                  Sed
                                                                                                                                   protein,
                                                                                                                                  secreted
                            ВР
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2000US-0184664P.
2000US-0184564P.
2000US-0186350P.
2000US-0189874P.
2000US-01980274P.
2000US-020967P.
2000US-02164886P.
2000US-02164886P.
2000US-02164886P.
2000US-0216488P.
2000US-021648P.
2000US-021648P.
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2000US-021648P.
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2000US-0225264P.
2000US-0225264P.
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2000US-0225213P.
2000US-0225264P.
2000US-0225213P.
2000US-0225213P.
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2000US-0225213P.
2000US-0225759P.
2000US-0225759P.
2000US-0225759P.
2000US-0229343P.
2000US-0229344P.
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2000US-0229344P.
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2000US-023943P.
                             454
                                                                                                                                  novel
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                             CDNA;
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                                                                                               (first
                                                                                                                                   encoding
                            standard;
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24-FEB-2000;

22-MAR-2000;

16-MAR-2000;

17-MAR-2000;

17-MAR-2000;

18-APR-2000;

19-MAY-2000;

10-JUL-2000;

11-JUL-2000;

11
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         AAS26590
ID AAS26590
                                                              AAS26590
                                                                                                                                   Human
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosting a pathological condition or susceptibility to a set of pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunosasays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiox arrest, carebral ischaemia, angiogenssis, neoplasms of the breast or liver, cardiovascular disorders e.g. carebral ischaemia, angiogenssis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders e.g. Alzheimer's disease, infections caused to be used to aid wound healing and epithalial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The primted sequence encodes a novel secreted protein of the printed the printed
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1.9e-157;
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Pred. No. 1.9e
0; Mismatches
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diagnosing, preventing, treating or ame
used as food additives or preservatives
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 2000US-0249265P.
2000US-0249297P.
2000US-0249300P.
2000US-0250160P.
2000US-025130P.
2000US-0251988P.
2000US-0251988P.
2000US-0251988P.
2000US-0251868P.
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2000US-0251868P.
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il Similarity 99.8%;
416; Conservative
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P-PSDB; AAU16603.
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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2000US-0180628P.
2000US-0214886P.
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2000US-0217487P.
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2000US-0229344P.
2000US-0229343P.
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2000US-02334274P.
2000US-023423P.
2000US-023423P.
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                                                                                                                                                                                                                                                  polynucleotide
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                                                                                                                                                                                       DNA;
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28-JUN-2000;

07-JUL-2000;

07-JUL-2000;

11-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

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Berghs C, Rothenberg ME, Guo
Kekuda R, Ji W, Miller CE;
Liu X, Padigaru M, Alsobrook JF
             TTCAAACATGCGCCAAAGAAGTCTTGCAATACCTCTCCCG
                                                                                     New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOV and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
                                                                                                                                                              Gorman L, Ellerman K, Catterton E, Shenoy SG, L Burgess CE;
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Vernet CAM,
A, Leach MD, C
Taupier RJ, S
Edinger SR, B
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Gerlach VL,
Shimkets RA,
Rieger DK, T
Lepley DM, E
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m, muscular,
nary, cardiova
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d. No. 1.9e-157;
Mismatches 1;
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ting e.g. neural, immune s
tive, gastrointestinal, g
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2000US-0237039P.
2000US-0237039P.
2000US-0237040P.
2000US-0237040P.
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2000US-0241785P.
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2000US-0241809P.
2000US-0241869P.
2000US-0251868P.
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Best Local Similarity 99.8%;
Matches 416; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM,
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ABU55671.
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RUBEN S M
BARASH S
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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02-OCT-2000;
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P-PSDB;
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                                          The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polymucleotide is useful for treating endocrine/ metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. psoriasis, allergy, lupus erythematosus, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus, esteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, casthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), lung diseases (enghysease in the colon, lung, liver diseases (e.g. liver, prostate or brain cancers, or melanoma), liver diseases (e.g. liver, cirrhosis), lung diseases (emphyseme or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic trials. This sequence encodes a novel human NOV protein
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                                                                                                                                                               autoimmune
erythematosus
                                                                                                                                                                                                                                                  functional
                                                               syndrome
                                                                                                                                                                                                     arian,
liver
disease),
parasitic).
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gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
primer; probe.
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                                                                                                                                                                                                                                                                                                                    T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                          Score 342; DB 10;
Pred. No. 1.9e-146;
0; Mismatches 1;
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                          English
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                        20; Page 125-126; 586pp;
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nes 392; Conservative
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The invention comprises compositions used for the therapy and diagnosis of ovarian cancer. The compositions comprise one or more ovarian tumour proteins, their associated polynucleotides, or immunogenic portions of the proteins. The ovarian tumour polynucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549 represent human ovarian tumour protein cDNA clones
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Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Cordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Irownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Irownstein, M.J., Bosak, S.A., McEwan, P.J.,
Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Ile, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Ile, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Ling, M., Madan, A., Young, A.C., Shevchenko, Y.,
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Odriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Clone distribution: MGC clone distribution information through the I.M.A.G.E. Consortium/LLNL at: http://image Series: IRAL Plate: 42 Row: f Column: 3
This clone was selected for full length sequencing becapassed the following selection criteria: GenomeScan gen prediction.
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Eukaryota; Metazoa; Chordata;
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Department cine, One Worley, K.C.

Direct Submission
Submitted (05-FEB-2000) Human Genome Sequencing Center, of Molecular and Human Genetics, Baylor College of Medi Baylor Plaza, Houston, TX 77030, USA

REFERENCE AUTHORS TITLE

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Department cine, One 101 Worley, K.C.

Direct Submission
Submitted (30-NOV-2000) Human Genome Sequencing Center, of Molecular and Human Genetics, Baylor College of Medi Baylor Plaza, Houston, TX 77030, USA
On Nov 30, 2000 this sequence version replaced gi:10945
INFORMATION: http://www.hgsc.bcm.tmc.edu/or email gc-help@bcm.tmc.edu

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only cof CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

searches, and 550) s GDB,

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P. Green and

BLAST the are not by E led by -34) to exons ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550)

of a local database that includes entries from dbSTS, GDB, local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34)

EST and cDNA sequences. Genes demonstrate at least two exo flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are identical matches are annotated as similar. SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

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| 9 89793 gcattttggg (a) ggctgaggtg 9 89828 gtctggtagt(t) tgagaccagc 9 89865 aacccatct(c) tacaaaaat 10 6179 gggccccaaa (a) tcactaagct 10 6179 gggccccaaa (a) tcactaagct 10 6220 aactgcttgg (g) gcaaactgct 10 6221 caaactgct (g) ggaactgctt 10 6540 aactgcttgg (g) gcaaactgct 10 6540 caactgct (g) gaaactgct 10 6540 caactgct (g) caaactgcc 10 7029 ggttggaaggt (g) aaggggaag 10 7087 ggttggaaggt (g) aaggggaag 10 7086 gagagaagac (a) agagggaag 10 7087 gagagaagac (a) agagggaag 10 7086 gagagaagac (g) agagggaag 10 7087 gagagagaac (g) agagggaac 10 7101 gagaggaaca (g) agagggaac 10 7102 gagagaacaa (g) agaagtgcca 10 7103 gagaggaacaa (g) agaagtgcca 10 7104 gagagaaaggg (a) aaagtgccac 11 7105 gaagggaacaa (g) agaagtgccac 11 7105 gaagggaacaa (g) agaagtgccac 11 7105 gaagggaacaa (g) agaagtgccac 12 7105 gaagggaacaa (g) aaagtgccaca 13 7105 gaagggaacaa (g) aaagtgccaca 14 7105 gaagggaacaa (g) aaagtgccaca 15 7105 gcaaaaggga (g) aaagtgccacacat 16 7105 gaagggaacaa (c) cacaagaata 17 76 78; Score 1159; DB 9; Length 204228; | Matches 1159; Conservative 0; Mismatchers 159; Conservative 0; Mismatchers 353 GGGAGCGATCTCTGAAATCGCCCATTCAGTCCGGAGGGAG  | QY         473 GAGCCGCGGTGTGTCCAGCTGATCAACCACTTGCACGCGGTGGCCACCCAGTTCTTGCCC         532           Db         44867 GAGCCGCGGTGTTGTCAACCACTTGCACGCGCGCGCCACCCAGTTCTTGCCC         4808           QY         533 ACCCCGCGGTGTTGTCAACAGGTCCTTCTGAGCAAAGGCACCGGCGCTCCTCGGCC         592           QY         593 GCCGGGTGTGTTGACTCAACAGGTCCTTCTGAGCAAAGGCACCGGCGCTCCTCGGCC         4748           QY         593 GCCGGGTCGTGTTGACTCAACAGGTCCTTCTGAGCAAAGCTCGGAGCTCCTCGGCC         652           QY         653 TACTGCGTGCCGCCCCTGCTGGAGCGCGGGGGCAGAAGCTCGGAGCCCTCGCC         652           QY         653 TACTGCGTGCCGGCCCCCTGCTGGGGGCGGGGCGAGAAGCTCGCCGCGGGGCCCTCGCCTCGCCTCGCCTCGCCCTCGCCCTGCCTGGGGGCCGAGAACGCTCGCCGGGGCCCGAGAACGACTCGCCCGGGGCCCGAGAACGCTCGCCGGGGCCCGAGAACGCTCGCCGGGGCCCGAGAACGCTCGCCGGGGCCCGAGAACGCTCGCCGGGGCCCGAGAACGCCCGGGGCCCGAGAACGCCCGGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGG   | 833 GCGCCCAAGAGGATGAAGCTGGATTCCCGCGGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGG  |

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Patent: WO 02068579-A 13000 06
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
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AY20420.

Canis familiaris (dog)

Canis familiaris

Sukaryota; Metazoa; Chordata; Craniata; Velucanis familiaris

Bukaryota; Metazoa; Chordata; Carnivora; Fissipedia; Canidae; Canidae
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Ovarian tumor-associated sequences
Patent: WO 0151513-A 1045 19-JUL-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 1045 from Patent WO0151513
AX198590
AX198590.1 GI:15388911
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Mammalia; Eutheria; Primates
    CORPORATION (US)
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Vertebrata; ; Hominidae;
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 40773 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liew, C.C., Marshall, W.E. and Zhang, H. Compositions and methods relating to osteoarthritis Patent: WO 02070737-A 32889 12-SEP-2002; Chondrogene Inc. (CA)
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32889 from Patent WO02070737.
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/organism="Homo sapiens"
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/organism="Homo sapiens
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Mammalia; Eutheria; Primates;
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Mammalia; Eutheria; Primates;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Catarrhini; Hominidae;
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 32086 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liew, C.C., Marshall, W.E. and Zhang, H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 33680 12-SEP-2002;
Chondrogene Inc. (CA)
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Sequence 33680 from Patent WO02070737.
CQ688754 GI:42221719
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/db_xref="taxon:9606"
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Primates;
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| δý         | 961 CGCCCAAGAGGATGAAGCTGGATTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGGGG                       |
| ΩD         | AGAGGATGAAGCTGGATTCCCGCGGCGGCGGCAGCGGCGGCGGCGCCCGGGGGG                                     |
| Oy .       | 1021 GCGCGGCGGCGGCGCCGCCTTCTGGGGCCCGACCCTGCCGCGCGCG  |
| QQ         | scedcedcadcadcatratedadcacadaacataaaaaaaaaaaaaaaaaaaaaaaa                                  |
| δλ         | 1081 TGAGACCCGACGCCCCTGCTCAGCTCGCTGGTGGCGTTCGGCGGAGGCGGAGGCGCGCGC                          |
| gg         | sacgcccccrccrcacrcccrccrccrccrrcccrrcccccccc   |
| λŏ         | 1141 CCTTCCCGCAGCCCGCGCCGCCGCCCCCTTCTGCCTGCCCTTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC |
| ΩΩ         | SAGCCCGCGCCGCCGCCCCTTCTGCCTGCCTTCTGCTTCTCTCTCTCTCTCTCTCT                                   |
| ογ         | 1201 CTTCTGCAGCTGCCGCCTACGTGCAGCCCTTCCTGGACAAGAGCGGCCTGGAGAGTATC 1260                      |
| අුු        | GCTGCCGCCTACGTGCAGCCCTTCCTGGACAAGAGCGGCCTGGAGAAGTAT  |
| ٥'n        | 1261 IGTACCCGGCGGCGCCCCCCTTCCCGCTGCTATACCCCGGCATCCCCGCCCG                                  |
| qq         | scededededecededificadetadratacededearecedede  |
| δ.         | CGGCAGCCGCGCCAGCCGCCGCCGCCGCCGCCGCCGCCGC   |
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| δλ         | 1381 CCTCGGTGTTGTCGCCCCCTCCCGAGAAGGCGGCGCCGCCGCGCGCG                                       |
| qa         | rrerceccccrccadaageceecccccccadaccccccccccccccccc  |
| QY         | 1441 ACGAGGIGGCGCCCTTGGGGCGCCGCACCCCCAGCACCGCACGGCCGCACCCACC                               |
| qq         | seeceectradeceeceeceeceeceereeceeceeceeceeceecee   |
| ,<br>VO    | 1501 CCTTCGCCGGGGCCCCGGGGGAACCCGGAGGTCTTGCTCAGGAAGATCCCTCGC 1560                           |
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| Qy         | 1621 GAGAAGTTAAAATACCCTTAAGGAGGTTCAAGCAGAGTGAGAAGTTAAAATACCCTTAAG 1680                     |
| qq         | AAATACCCTTAAGGAGGTTCAAGCAG   |
| Qy         | 1681 GTCTTTAAGGGAAGTGTAATAGATGCACGACAGGCATAAACAAGAACAACAAAAAGG 1740                        |
| අු         | ggaggaagtgtattagtgcacgacaggcataaacaagacaaaa  |
| δ          | 1741 GIGITAIGIGIACATICGGAGTICCIGITITIGCICATCCCGCACCCCCCCCCC                                |
| ДQ         | rdnáckartodakatrociáritrácickárocádakokockockocítok  |
| ζζ         | 1801 CACTAACATCCCTTTCTTCCCCCCACCAGCTGTAAAAGATCCTATGCGAAAGACACTGGC 1860                     |
| ΩD         | recerricinececedadergrahahaharechargeahadaea   |
| ò          | 1861 TCTTTTTTTAATCCCCCAAATAAATTTTGCCCCCTTTTAGGCCATGTTCCATTATCTCT 1920                      |
| QC         | PTAATCCCCCAAATAAATTTTGCCCCCTTTTAGGCCATGTTCCATTAT   |
| <i>⊼</i> 0 | 1921 TAAAATTGGAACCTAATTCGAGAGGAAGTAAGAAGGGTCTGTTCTGTGGCTGAGCTAGGT 1980                     |
| Ωp         | saacctaatrcgagggaggrangaagggrcfgtrcfgfggcrgagcr  |
| δ          | GAACCCCGGGGTAGGGGAAAGATGTTAACACCTTTGACGTCTTTGGAGTTGACATGGAAC 204                           |
| Dp         | segracecaaacargiraacaccirreaccirriscacirriscacriscar                                       |

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WPI; 2002-723277/78 P-PSDB; ABG96308.

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

186-187; 481pp; English. Disclosure; Page

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as particular use with patients having an enhanced risk of developing ovarian cancer. The cancer markers may be used in the management and treatment of e.g. patients having a familial history of ovarian cancer. The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. brain and central nervous system disorders (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatous orchitis), testicular cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian cancer as selecting a composition of a compound, or inhibiting ovarian cancer cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the 

Sequence 3641 BP; 994 A; 922 C; 836 G; 889 T; 0 U; 0 Other;

ö 120 120 180 180 240 240 300 300 360 360 420 ATCTGA AACAGCAGTTGAACATGGACGAAGGAATTCCTCATTTGCAAGAGAGACAGTTACTGGAACACAACAGTTACTGGAACACAGCAGTTACTGGAACACAGCAGCAGAGGAATTCCTCATTTGCAAGAGAGACAGTTACTGGAAC AATTGACAACTCTGGGACATCTGGAGAAGCTGTAGTCTTGGAATTAACTTTGAAACACT GGAGCA CTGCACTGAAGAGGGAGAGAGAGAGAGACTGGAGACGCACAGATCCCCCCAAGGTCTT AGAAAA Gaps Length 3641; TGCACTGAAGAGGAAGAGCGAGAGAGAGACTGGAGACGCACAGATCCC Indels TGAAACGAGACGACACCAAGGATACCTACAAATTACCGCA ; 0 DB 6; Score 3641; Pred. No. 0; ; Mismatches 0 Query Match Best Local Similarity 100.0%; Matches 3641; Conservative 0 61 Н 61 121 121 181 181 241 241 301 301 361 qq d  $\delta$ 8 В  $\delta$ ઠ

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| Db          | 361 AATTGACAACTCTGGGACATCTGGAGAAAGCTGTAGTCTTGGAATTAACTTTGAAACACT 420   |
|-------------|--|
| ò           | 421 TAAAAGCTTTAACCGCCTTAACCGAGCAACAGCATCAGAAGATAATTGCTTTACAGAATG 480   |
| QQ          | ACCGCCTTAACCGAGCAACAGCATCAGAAGATAATTGCTTTACAGAAT   |
| δλ          | 4,   |
| Ор          | yrcrcraaahcacccarrcaarccaarrcaarraaaracarrccacrcaarr   |
| δλ          | 541 AAACATGCGCCAAAGAAGTCTTGCAATACCTCTCCCGGTTTGAGAGCTGGACACCCAGGG 600   |
| qq          | sccaaadaadroniddaaracciciciccegiriidadagcidgacaccid  |
| δλ          | AGCCGCGGTGTCCAGCTGATCAACCACTTGCACGCCGTGGCCACCCAGTTCTTGCCCA 66  |
| Ср          | grerereaecrearcaaccactrecacecereeceaccaccaerreres  |
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| λο <i>τ</i> | ACTGCGTGCCCGTCATCCAGCGGACTCAGCCCAGCGCCGAGCTCGCCGCCGAGACGACA 8  |
| QQ          | ACTGCGTGCCCGTCATCCAGCGGACTCAGCCCCGAGCTCGCCGCCGAGAACGACA 84   |
| δλ          | GACAGCGGCTACGGCGGCGAAGCCGAGGCCCGGCCGGACCGCGAGAAGGCA 90   |
| QQ          | ccacacccccataccccccccaaccccaccccccccccc  |
| ٥'n         | 901 AAGGCGCGGGGGGGGCGCGTCACCATCAAGCAGGAGCCTCCCGGGGAGGACTCGCCGG 960   |
| Dp          | 1 AAGGCGCGGGGGCGAGCCGCGTCACCATCAAGCAGGAGCCTCCCGGGGAGGACTCGCCG  |
| δ           | 961 CGCCCAAGAGGATGAAGCTGGATTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGGGGGGG  |
| Ор          | AGAGGATGAAGCTGGATTCCCGCGGCGGCGGCAGCGGCGGCGGCGGCGGGGGGG   |
| δλ          | 1021 GCGCGCGCGCGCGCCAGCCGCGCTTCTGGGGCCCCGACCCTGCCGCCGCGCGCCGCGCGCTGC 1080                                      |
| Ωp          | cegcaeccecectroreseccceaeccrecteccecececece  |
| Ολ          | ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC   |
| QQ          | saccccccccrccrccrccrccrccrccrccrccrrcccrcccc   |
| ٥x          | CAGCCCCCCCCCCCCCCTTCTGCCTGCCCTTC   |
| qq          | scechecccececececececececececericies   |
| δ           | SCTGCCGCCTACGTGCAGCCCTTCCTGGACA  |
| QQ          | AGCTGCCGCCTACGTGCAGCCTTCCTGGACAAGAGCGGCCTGGAGAGTAT   |
| δλ          | CGGCGGCTGCCGCCCGTTCCCGC  |
| QQ          | segoegerecoeccoerrocoecrecraracocoeces de la consecoecce   |
| δλ          | 1321 CGGCAGCCGCGCCGCCGCCGCCGCTGCCGCCGCCGCCGCCGCGCTTCCCCTGCTG   |
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| ٥'n         | rrgrcg   |
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| ٥y          | 1441 ACGAGGTGGCGCCCTTGGGGCGCCGCACCCCCAGCACCCGCACGCCGCACCCACC   |

| 261 ACMANACACACACACACACACACACACACACACACACACA  |
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| DP<br>DP          | 1441 ACGAGGTGGCGCCCTTGGGGCGCCCCCCCCCCCCCCCCC                             | op ox  | aaaaacaacaacaaaaaacaagtcc<br>                |
|-------------------|--|--|--|
| Qy<br>Db          | AGCTCCCTGAATCCTTGCGTCCCGAAGGACGGAGGTTCAAGCAGAGT 1                        | ව රු   | caaaagtgaacgaaagcatttaac<br>                 |
| Qy                | CCCTTAAGGAGGTTCAAGCAGAGTGAGAAGTTAAAATACCCTTAAG 168                       | , d  | 2701 AGAATGAAGTCCTGTGAGGCCTTCCTATCTCCAAG<br> |
| Š G               | GAAGTGTAATAGATGCACGACAGGCATAAACAAGAACAACAAAAACAG 1740<br>                | Qy<br>Dp   | 2761 CAGATACCAGATAATCACAAAGAAAGCTTTTTTAA<br> |
| Qy<br>Qu          | TTCGGAGTTCCTGTTTTGCTCATCCCGCACCACCCCACC                                  | QY<br>Dp   | 2821 AGATATTTTAGTTTGTTGCCAAGGTAGCACTGTG<br>  |
| Š 9               | rcttcccccaccagctgtaaagatcctatgcgaaagacactggc 186                         | Qy<br>Db   | 2881 AGGGGTGAGACACAGTCTGACTATGAGTGAGG        |
| oy<br>Ob          | CCCCAAATAAATTTTGCCCCCTTTTAGGCCATGTTCCATTATCTCT 192<br>                   | oy<br>Dp   | 2941 TTGGTGCATTTGCTGCTGCTGTTGCTACTGTTTGC<br> |
| λ <sup>ο</sup> dd | 1 TAAAATTGGAACCTAATTCGAGAGGAAGTAAGAAGGGTCTGTTCTGTGGCTGAGCTAGGT 198       | Qy   | 3001 TAAACTCTTAGCCTACAAGGTGGCTCTTATGTACA<br> |
| Qy<br>Dp          | 981 GAACCCGGGGTAGGGAAAGATGTTAACACCTTTGACGTCTTTGGAGTTGACATGGAAC 204       | Qy<br>Dp   | 3061 ATGTCTGACATGCTATTTTTGTAGGGAGAAATAT<br>  |
| y du              | 41 AGCAGGTAGTTGTTATGTAGAGCTAGTTCTCAAAGCTGCCCTGCCTG                       | දු දු  | 3121 TATCTTTGGGGAGGATTTGCTGAAAAGTTGCACT<br>  |
| දු දු             | TGAGGCTCTTTTTAGAATTGAATTTACTCTTCAGTATTTCTAATGT 216                       | රු යු  | 3181 CAAGCTTATGCTGTCTTAAATTATTTTAAAAAAT      |
| Qy<br>Dp          | AGGCATATATTTTCAAAGAAGTGAGGATGCAGTTTCTCACGTTGCA 222                       | os<br>So<br>So<br>So<br>So<br>So<br>So<br>So<br>So<br>So<br>So<br>So<br>So<br>So | 3241 TGGTTTAGAAAGTTTAGTATGTGACGATAAACTA<br>  |
| λο, qa            | ACCTATTCTGAAGTGGTTTTAAATGGTATCTCTTAGTAACTTGCACTCGTTAAAGAAACA 228         | O<br>Dp  | 3301 TTCAGCACTCCATAAATTCTATTACCTAAATATTG<br> |
| S S               | 281 GGAGCTGGGCCATCGTCAGAACTAAGTCAGGAAGGAGATGGGATGAGAAGGCCAGAATCA 234<br> | රු අු  | 3361 TCTTACTAAGGAATAAAACTTTAATATACGATAT<br>  |
| , do qa           | CTAACACTTTATTGAGAAATTGACCATGAATTAATGGACTCATCT 240                        | cy<br>GD   | 3421 CATAATGGATGCTCAATTAGTTTTAAGATATCTAT<br> |
| λο qα             | TAAGTCCATATATAGATAGATATCTATCTGTACAGATTTCTATTTATCCA 246                   | රු පු  | 3481 GTTCTCAGATTTACACCTTTTTTTTGTCATTGGCT<br> |
| QY                | 461 TAGATAGGTATCTATACATACACATCTCAAGTGCATCTATTCCCACTCTCATTAATCCAT 252     | <u>کې</u> وو   | 3541 GCAAGCCTCCAGGCTCTGGCTTTGTCTACCTGCTC     |
| QV<br>Dp          | 1 CATGTTCCTAAATTTTTGTAATCTTACTGTAAAAAAGTGCACTGAACTTCAAAACAAA 258<br>     | λ<br>60 ·  | 3601 TGCAAAAGAAAACCTACCAATTAAAAAAAAAAAAAAAAA |
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ACTGATATATCCTATATTCTGTTAAAA CATAGTTGTTAATACATCCAATTAATG AGTCTATGTATTTTCTGGAGACCAAAC AATAAGGCTTAAACCAAGACCTTGTCT ATTAAATACTGTCTGTGAGAAACCAGC CTTTTGTTACAATGCTTATGCTTGGTA TAGAAATTACCTTTATATTCTAGTATT TCGTTCCCAATGTATCTTAATGAAAG AAAAAAA |||||||| |||||||

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AAACATGCGCCAAAGAAGTCTTGCAATACCTCTCCCGGTTTGAGAGCTGGACACCCAGGG
                                                                                                                         cccccaagctgttgactcaacaggtccctctgagcaaaggcaccggcgctccctcggccg
                                                                                                                                                                           ACGAGGTGGCGCCCTTGGGGCGCGCGCACCCCAGCACCCGCACGGCCGCACCCACCTGC
                        CAGAAGATAATTGCTTTACAGAATG
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                                                                                                                                                                                                                                    The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a compositifor diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                           Wood
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r treating psoriasis
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                                                                                                                                                           Williams PM,
                                                                     gene therapy; psoriasis; diagnosis
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pharmaceutical composition for diagnosing or
mammal.
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larity 100.0%;
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                                                          cDNA sequence
                                              entry)
                                                                      gene; antipsoriatic;
                      standard; cDNA;
                                                                                                                                                GENENTECH INC
                                              (first
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P-PSDB; ADN05014.
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Best Local Similarity
Matches 3641; Conser
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                                                                                               WO2004028479-A2
                                                          Antipsoriatic
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                                              01-JUL-2004
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Wu TD;
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| ACTAAATTTTTGTAATCTTACTGTAAAAAAAGTGCACTGAAC AACAACAACAACAAAAAAAAAGTCCAAACTGATATTCCTATA AACAACAACAACAAAAAAAAAGTCCAAACTGATATTTTTTTAATGC AGTGAACGAAAGCATTTAACTGGCCAGTTTTGATTGCAAATGC AGTGAACGAAAGCATTTAACTGGCCAGTTTTGATTGCAAATGC AGTCCTGTGAGGCCTTCCTATCTCCAAGTCTATGTATTTTCT AGTCCTGTGAGGCCTTCCTATCTCCAAGTCTATGTATTTTCT AGGCCTTCCTATCTCCAAGTCTATGTATTTTCT AGGCCTTCCTATCTCCAAGTCTAAAGCCTTAAACCAA |   | OY  2941 TTGGTGCATTTGCTGCTGTTGCTACTGTTTGCCTCAAACGCTGTGTTTAAACAA     | Db 3061 ATGTCTGACATGCTATTTTTGTAGGAGAAATATGTGCTAATGATATTT  Qy 3121 TATCTTTTGGGAGGATTTGCTGAAAAGTTGCACTTTTGTAGCTT  Db 3121 TATCTTTTGGGAGGATTTGCTGAAAAGTTGCACTTTTGTTACAATGCTT  Db 3121 TATCTTTTGGGAGGATTTGCTGAAAAGTTGCACTTTTGTTACAATGCTT | OY 3181 CAAGCTTATGCTGTCTTAAATTATTTTAAAATTAATTAAT                         | OY 3301 TTCAGCACTCCATAATTCTATTACCTAAATATTGCCACACTATTTTGTGATTTAA        | Qy         3421 CATAATGGATGCTCAATTAGTTTTAAGATATCTATAACTATAGGGATACAAATCAGGATACAAATCAGGATACAAATCAGGATACAATCAGGATACAATCAGGATACAATCAGGATACAATCAGGATACAATCAGGATACAATCAGGATACAATCAGGATACAATCAAT | Qy         3541 GCAAGCCTCCAGGCTCTGGCTTTGTCTACCTGCTCCTTCCCAATGTATCTT           Db         3541 GCAAGCCTCCAGGCTCTGGCTTTGTCTGCTCGTTCCCAATGTATCTTTGTCTTGTCTTCCTGCTTCCCAATGTATCTTTGTCTTGTCTTCCTGCTTCCCAATGTATCTTTTTTCTTCTTCTTCTTTTTTCTTCTTTTTTTT |
|--|---|---|--|--|--|---|---|
|  | 8 4 7 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 861 TCTTTTTTTAATCCCCCAAATAAATTTTGCCCCCTTTTAGGCCATGTTCCATTATCTCT 192 | 1981 GAACCCCGGGGTAGGGGAAAGATGTTAACACCTTTGACGTTTTGGAGTTGACATGGAAC 2040 [  | 2101 TCCACAAACAGATTGAGGCTCTTTTTAGAATTGAATTTACTCTTCAGTATTTTCTAATGT 2160 [ | 2221 ACCTATTCTGAAGTGGTTTAAATGGTATCTCTTAGTAACTTGCACTCGTTAAAGAAACAC 2280 | 2341 TTCCTAGTACATTTGCTAACACTTTATTGAGAATTGACCATGAATTAATGGACTCATCT 2400 [   | TCTATT<br>      <br> CTATT<br>  |

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with invention also relates to nucleic acid of the invention; the crecombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of upolymuleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polymuleotide probes invention; methods for the identification of compounds that modulate the analyor monoclonal antibodies for carrying out the methods of the invention or activity of the polymuleotide and/or polypeptide; and 767 cantig sequences corresponding to the coMA sequences of the invention are corresponding to the coMA sequences of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the invention of mutations responsible for general diseases or their and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alaheimer's discusse and other neurodegenerative diseases, and in the recombinant production of a protein. The polypeptides of the protein of a protein. The polypeptides of a protein. The polypeptides of the invention are used for treating diseases, and and an and in the recombinant production of a protein. The polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
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tostatic;
                                                                                                                                                                      gene mapping;
Alzheimer's disease
disorder; wound; bu
                                                                                                                                                                 Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease neurodegenerative disease; anaemia; platelet disorder; wound; kulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; noot neuroprotective; antianaemic; anticoagulant; thrombolytic; vulne antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytgene therapy; gene; ss.
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                                 standard; cDNA; 3521
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Wang D,
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P-PSDB; ADC31646.
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Ghosh M,
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Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                      WO2003029271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2002;
                                                                                                                                         Human novel
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are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                        TAAAAGCTTTAACCGCCTTAACCGAGCAACAGCATCAGAAGATAATTGCTTTACAGAATG
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No. 0;
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Best Local Similarity 99.9%;
Matches 3392; Conservative
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T, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP;
Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog F.
Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;
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ATGTCTGACATGCTATTTTTGTAGGGAGAAAATATGTGCTAATGATATTTTGAG
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The invention relates to an isolated polypeptide, designated NOVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polymucleotide or an antibody created from the protein, its useful in the manufacture of a medicament for treating a syndrome associated with a human diseasent by NOVX-associated disorder, or for treating or preventing a NOVX-associated disorder in a subject, preferably human. The isolated protein, its encoding polynucleotide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, and various disorder; immune disorders, haematopoletic disorders associated disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with choseity, the metabolic syndrome X, wasting disorders associated with antibody created from the protein are useful for treating or preventing neurological disorders such as espilepsy, stroke, mental disorders including mood, anxiety, schizophrenic disorders, disorders of vesicular transport such as cystic fibrosis, diabetes mellitus, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid architis, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid architis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynucleotide of the invention and be used to treat disorders by gene therapy. This polynucleotide sequence represents the DNA encoding one of the isolated
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Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis; lung disease; emphysema; obstructive pulmonary disease; haemophilia; stroke; infection; gene; ss.
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WPI; 2003-313242/30 P-PSDB; ABO14645.

(NOVX) New cytoplasmic, nuclear membrane bound or secreted polypeptides (NO' and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia stroke or infections.

20; Page 125; 586pp; English Claim

The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polynucleotide is useful for treating endocrine/

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metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus, asthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (emphysema or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic analysis of varions, and for monitoring the effects of drugs during clinical trials. This sequence encodes a novel human NOV protein
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basic helix loop helix protein; cell differentiation; proliferation;
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                                                                                                            The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
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15-MAY-2000;
09-JUN-2000;
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The present invention relates to a microarray comprising a matrix of at least one cDNA probe from a set of probes immobilised to a solid surface in a predetermined order, where a row of pixels corresponds to replicates of one distinct probe from the set. The probes are complementary to nucleic acid sequences that are expressed differentially in aggressive as compared to non-aggressive types of clear cell renal carcinoma (CC-RCC) and that hybridise to the probes under high stringency conditions. The microarray is useful for the prognosis of patients with CC-RCC, wherein aggressive and non-aggressive CC-RCC tumour types are characterised by differential expression profiles of genes that hybridise with one or more probes immobilised on the microarray. The arrays are useful for gene expression profiling of tumour and normal tissues. The present sequence represents a human cDNA sequence up-regulated in CC-RCC patients
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                                                                                                                                                                                                                                                                                                                        Human; microarray; solid surface; immobilised probe; CC-RCC; differential expression profile; aggressive CC-RCC tumour type; non-aggressive CC-RCC tumour type; clear cell renal carcinoma; gene expression profiling; tumour tissue; gene; ss.
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useful
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Pred. No. 2.5e-194;
); Mismatches 0;
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ATACATCCAATTAATGATGTCTGACATGC
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Best Local Similarity 100
Matches 552; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection;
                                                                                                                                                                                                                                                               acid sequences may be useful in diagnostic and screening applications The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                            CGTTAAACTCTTAGCCTACAAGGTGGCTCTTATGTACATAGTTGTTAATACATCCAATTA
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                                                                                 Score 516; DB 12;
Pred. No. 4.9e-181;
; Mismatches 0;
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Best Local Similarity 99.8%;
Matches 636; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                              tissue sarcoma-upregulated DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue
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ADQ24375
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2000US - 0234997P.
2000US - 0234998P.
2000US - 0235484P.
2000US - 0235484P.
2000US - 0235834P.
2000US - 0235836P.
2000US - 0235836P.
2000US - 0236363P.
2000US - 024096P.
2000US - 024096P.
2000US - 0246523P.
2000US - 0246528P.
2000US - 0246611P.
2000US - 0246613P.
2000US - 024920P.
2000US - 024920P.
2000US - 024920P.
2000US - 0249214P.
2000US - 0249218P.
2000US - 0249219P.
2000US - 024929P.
2000US - 0251989P.
2000US - 0251989P.
2000US - 0251989P.
2000US - 0251999P.
 25-8EP-2000;
27-8EP-2000;
27-8EP-2000;
27-8EP-2000;
29-8EP-2000;
29-8EP-2000;
29-8EP-2000;
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20-0CT-2000;
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05-05C-20
06-05C-20
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08-05C-20
08-05C-20
     additive;
       food
        skin ageing;
      proliferation;
         epithelial cell gantiproliferative
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2000US - 0184664P.
2000US - 0186350P.
2000US - 0186350P.
2000US - 0189812P.
2000US - 019812P.
2000US - 019812P.
2000US - 0209467P.
2000US - 0209467P.
2000US - 0218480P.
2000US - 022526P.
2000US - 022526P.
2000US - 022526P.
2000US - 0225214P.
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2000US - 022934P.
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2000US - 022934P.
2000US - 0231414P.
2000US - 0231414P.
2000US - 0231414P.
2000US - 023239P.
2000US - 023423P.
                                                                                                                                                         2001WO-US001341
         wound healing;
preservative;
                                                                                          WO200155322-A2
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24-FEB-2000;

26-MAR-2000;

16-MAR-2000;

17-MAR-2000;

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18-APR-2000;

19-MAY-2000;

19-MAY-2000;

10-JUL-2000;

11-JUL-2000;

14-AUG-2000;

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                                                                                                                                                                                      concided secreted proteins. The nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a latenological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (EDISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovassular disorders e.g. carebral isohaemia, angiogenesis, cerebrovassular disorders e.g. carebral isohaemia, angiogenesis, arrest, cerebrovassular disorders e.g. cerebral isohaemia, angiogenesis, can also be used to aid wound healing and epithelial cell proliferation, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, cransplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The princesent sequence encodes a novel secreted protein of the invention. Note: The sequence encodes a novel secreted protein of the printed.
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                                                                                                                    lles encoding 461 human
treating or ameliorat:
or preservatives.
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il Similarity 100.0%; E
496; Conservative 0;
                                                      Ruben
 2001US-0259678P
                             SCI INC
                                                                                                                        nucleic acid molecules
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used as food additives o
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P-PSDB; AAU16188.
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CCCGCAGCTGTTGACTCAACAGGTCCCTCTGAGCAAAGGCACCGGCGCTCCCTCGGCCG
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2000US-0217487P.
2000US-02264F18P.
2000US-0225268P.
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2000US-0225268P.
2000US-022524518P.
2000US-022524518P.
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                                                   standard; DNA;
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17-SEP-2000;
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23-SEP-2000;
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07-JUL-2000;
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                                                                                                                                                                                                                                                                                      Human novel
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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent human novel polynucleotides of the invention
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Pred. No. 1.4e-173;
0; Mismatches 0;
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Best Local Similarity 100.0%; E
Matches 496; Conservative 0;
2000US-0237039P.
2000US-0237040P.
2000US-0239935P.
2000US-0241785P.
2000US-0241785P.
2000US-0241809P.
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2000US-0251868P.
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RUBEN S M
BARASH S
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
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                                  CACTITATIGAGAAATIGACCAIGAATIAATGGACTCATCTTAATITCTTCTAAGTCCAT
2240 AAATGGTATCTCTTAGTAACTTGCACTCGTTAAAGAAACACGGAGCTGGGCCATCGTCAG
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Pred. No. 3.9e-149;
0; Mismatches 0;
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as a
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                                                                                                                                                                                           cancer
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30-MAY-2002;
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Berghs C, Rothenberg ME,
Kekuda R, Ji W, Miller
Liu X, Padigaru M, Alsobr
                                                                                                                                                                                                                                                                                                    Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disoablism-related disease; obesity; central nervous system disolism-related disease; Parkinson's disease; epilepsy; multiple scl schizophrenia; depression; autoimmune disorder; inflammatory disportasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis colon cancer; lung cancer; liver cancer; breast cancer; ovarian prostate cancer; brain cancer; melanoma; liver disease; liver ci lung disease; emphysema; obstructive pulmonary disease; haemophistroke; infection; gene; ss.
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atterton E,
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2002US-0324969P.
2002US-0373212P.
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Gerlach VL, Vernet CAM,
Shimkets RA, Leach MD,
Rieger DK, Taupier RJ,
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The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating to reating the protein is useful in gene therapy for treating to reating endocrine, polypeptide or polynucleotide is useful for treating endocrine, metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. posciasis, allergy, lupus erythematosus, asthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of drugs during clinical trials. This sequence encodes a novel human NOV protein
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Novel bHLH type transcriptional gene, DE BD011858.

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WO 0114551-A/1.

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Fukaryota; Metazoa; Chordata; Craniata;

Mammalia; Eutheria; Primates; Catarrhini

(bases 1 to 3641)

Fujimoto, K., Shin, M. and Kato, Y.

Novel bHLH type transcriptional gene, DE Patent: WO 0114551-A 1 01-MAR-2001;

CHUGAI PHARM CO LTD, KATSUMI FUJIMOTO, MEI

BD 01-MAR-2001

PP 19-JUN-2000 WO 2000JP003991

PR 19-JUN-2000 WO 2000JP003991

PR 19-AUG-1999 JP 99P 233286

PI KATSUMI FUJIMOTO, MEI SHIN, YUKIO KAT

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540 3540 3600 3480 3420 3480 3600 -JAN-2001 Euteleostomi o F CTACA Liberary 2 (bases 1 to 3641) Fujimoto, K. Direct Submission Submitted (31-MAY-2000) Katsumi Fujimoto, hiroshima university, department of biochemistry, school of dentistry; 1-2-3, kasumi, department of biochemistry, school of dentistry; 1-2-3, kasumi, minami-ku, hiroshima 734-8553, Japan (E-mail:kfujimo@hiroshima-u.ac.jp, Tel:81822575629, Fax:81822575629) TCTTACTAAGGAATAAAAACTTTAATATACGATATGATATTGTCTAATAATTAAAAAGA CAATCTCTT ., Shingu, S., and Kato, Y. 2, a new member 27 TTAAGATATCTATAACTATAGGGATACAAATCA Chordata; Craniata; Vertebrata; Eutel Primates; Catarrhini; Hominidae; Homo PRI cds. (2001 linear complete, Homo sapiens
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominida

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Fujimoto, K., Shen, M., Noshiro, M., Matsubara, K., Sh
Honda, K., Yoshida, E., Suardita, K., Matsuda, Y. and
Molecular cloning and characterization of DEC2, a
basic helix-loop-helix proteins
Biochem. Biophys. Res. Commun. 280 (1), 164-171 (2
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| Best Local Similarity 100.0%; Pred. No. 0;  Matches 3641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 CTGCACTGAAGAGGAGAGAGAGAGACTGGAGACGCACAGATCCCCCCAAGGTCTC 60 | 61 CCAAGCCTACCGTCCCACAGATTATTGTACAGAGCCCCAAAAATCGAAACAGAGAAACG 1 | Qy<br>   | Oy 181 ATAGAGATTTTATAGGACTGGACTATTCCTCTTTGTATATGTGTAAACCCAAAAGGAGCA 240<br>            | OY 241 TGAAACGAGACGACACCAAGGATACCTACAAATTACCGCACAGATTAATAGAAAAGAAAA 300<br> | Oy 301 GAAGACCGAATTAATGAATGCATTGCTCAGCTGAAAGATTTACTGCCTGAACATCTGA 360<br> | 361 AATTGACAACTCTGGACATCTGGAGAAAGCTGTAGTCTTGGAATTAACTTTGAAACACT 42<br> | 421 TAAAAGCTTTAACCGCCTTAACCGAGCAACAGCATCAGAAGATAATTGCTTTACAGAATG 48   | OY 481 GGGAGCGATCTCTGAAATCGCCCATTCAGTCCGACTTGGATGCGTTCCACTCGGGATTTC 540 |   | 601 AGCCGCGTGTGTCCAGCTGATCAACCACTTGCACGCGTGGCCACCCAGTTCTTGCCCA 66 | 661 CCCCGCAGCTGTTGACTCAACAGGTCCCTCTGAGCAAAGGCACC     | 721 CCGGGTCCGCGCCGCCCCTGCTGGAGCGCGCGGGGCAGAAGCT<br>              | OY 781 ACTGCGTGCCGTCATCCAGCGGACTCAGCCCGAGCTCGCCGCCGAGAACGACA 840  | 841 CGGACACCGACAGCGGCTACGGCGGCGAAGCCGAGGCCGGCC | 901 PAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                 | 961 CGCCCAAGAGGATGAAGCTGGGATTCCCGGCGGCGGCGGCGGCGGCGGCGGGGGGGG | GCCCAAGAGGATGAAGCTGGATTCCCGCGGCGGCGGCAGCGGCGGCGGCGGCGGGGGGGG               |

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| 3241 TGGTTTAGAAAAGTTTAGTATGTGACGATAAACTAGAAATTACCTTTATATTCTAGTATT 3300 3241 TGGTTTAGAAAAGTTTAGTATGTGACGATAAACTAGAAATTACCTTTATTATTCTAGTATT 3300 3301 TTCAGCACTCCATAAATTCTATTACCTAAATATGCCACCACTATTTTGTGATTTAAAAAT 3360 3301 TTCAGCACTCCATAAATTCTATTACCTAAATATGCCACCACTATTTTGTGATTTAAAAAT 3360 3361 TTCAGCACTCCATAAAATCTTTAATATACGATATTGCCACACTATTTTGTGATTTAAAAAAT 3360 3361 TCTTACTAAGGAATAAAAACTTTAATATATGCGATATTGTGCTAATAATTAAAAAAT 3480 3421 CATAATGGAATAAAAAACTTTAATATATGGATATGTGTAATAATAAAAAGA 3420 3421 CATAATGGAATAAAAAAATTTAAGATATCTAATAAAAAAAA   | BC025968 Homo sapiens basic helix-loop-helix domain contains mRNA (cDNA clone MGC:39365 IMAGE:4650325), complete BC025968.1 GI:19684063 MGC. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human)  Strausberg, Metazoa; Chordata; Cranithi; Hominidae Klausner, R.D., Feingold, E.A., Grouse, L.H., Nahenmen, C.N. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C. Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Walin, G.M. Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, J. Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuk Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.C. | Worley, K.C., Hale, S., Garcia, A.M., Gay, L. Villalon, D.K., Muzny, D.M., Sodergren, E.J. Fahey, J., Helton, E., Ketteman, M., Madan, Sanchez, A., Whiting, M., Madan, A., Young, Bouffard, G.G., Blakesley, R.W., Touchman, Dickson, M.C., Rodriguez, A.C., Grimwood, J. Butterfield, Y.S., Krzywinski, M.I., Skals, Schnerch, A., Schein, J.E., Jones, S.J. and Generation and initial analysis of more human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 1, 12477932  2 (bases 1 to 3431)  Strausberg, R. Direct Submission Submitted (18-MAR-2002) National Institut Gene Collection (MGC), Cancer Genomics Of Institute, 31 Center Drive, Room 11A03, 1USA  NIH-MGC Project URL: http://mgc.nci.nih.gontact: MGC help desk |
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through the I.M.A.G.E. Consortium/LLNL at: http://image.l.
Series: IRAL Plate: 42 Row: f Column: 3
This clone was selected for full length sequencing because
passed the following selection criteria: GenomeScan gene
prediction.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Best Local Similarity 99.9%;
Matches 3213; Conservative
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Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Biraege, K., Blankenburg, K., Bonnin, D., Bouck, J., Boweis, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burket, C., Carcon, T.F., Carter, M., Cavacos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Choi, D., Chacko, J., Chare, D., Chen, C., Coyle, M., Darborne, S.R., David, R., Davida, M., Darger, H., Dudh, H.J., Douthwalte, K.J., Darger, H., Davis, C., Coyle, M., Darborne, S.R., David, R., David, M., Darger, H., Dudan, Rochas, S., Durbin, K.J., Bantarte, K.J., Darger, H., Dudan, C.C., Coyle, M., Balla, C., Barching, S., Bacctto, M., Falls, T., Ferraguto, D., Edwards, C.C., Flagi, N. Ford, J., Sachabart, C., Edward, G.C., Flaggi, N. Ford, J., Sachabart, C., Edward, G.C., Flaggi, N. Ford, J., Sachabart, C., Edward, G.C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Karlova, J., Jay, Y., Johnson, R., Jolivet, S., Joudah, S., Karlova, J., Jay, Y., Johnson, R., Jolivet, S., Joudah, S., Karlova, J., Jay, Y., Johnson, R., Jolivet, S., Worvah, J., Kovar, C., Kratova, C.J., Kureshi, A., Luder, M., Miler, R., Murchell, T., Mohabat, K., Molton, M., Miler, R., Mutchell, T., Mohabat, K., Mohama, F., Mokenson, J., Moyen, N., Michell, T., Mohabat, K., Mohama, S., Moser, M., Mattin, R., Mitchell, T., Mohabat, K., Mohama, S., Moser, M., Mattin, R., Mutchell, T., Mohabat, K., Mohama, S., Moser, M., Mattin, R., Mutchell, T., Mohabat, K., Mohama, S., Moser, M., Mattin, R., Mutchell, T., Mohabat, K., Mohama, S., Morken, M., Stan, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, M., Saban, H., Saban, H., Saban, H., Saban, H., Saban, H., Shan, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Sabar, K., Washington, S., Walliams, A., Markin, R., Walliams, A., Washington, C., Watlingto

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COMMENT

S (bases 1 to 204228)

Worley, K.C.

Direct Submission

Submitted (05-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Worley, K.C.

Direct Submission

Submitted (30-NOV-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 30, 2000 this sequence version replaced gi:10945701.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

only r of GTH: This sequence does not necessarily represent the sert of this clone. Overlapping regions of clones are o and submitted once, so the sequence for the remainder t may be found in the record for the adjacent clones. the insert may be Overlapping clone Features listing LENGTH: entire insert sequenced CLONE

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the

P. Green,

EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html

QUALSTAT-REPORT-

00:34:03 kdurbin Exp \$id: bcm-qual-stats.cc,v 1.6 1998/10/27 kdurbin \$ Info Option 1.01

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Average error rate (BCM-Phrap es Fraction of Phrap values less th Number of consensus changing edinamber of N's in consensus:
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Clip end:
2905 quality: quality: missing invalid reads Num

Surrounding Sequence
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aattaataac(a) agggcagctg
ctggtagttt(g) agaccagctt
gacaatcaga(a) atgaacttaa
aatcactaag(c) taaagaaaa
ccactatcac(a) agaatagcat
gtcaggaaaa(t) gccatctgtt
tcaggaaaat(g) ccatctgtta
caggaaaat(g) ccatctgtta
attaataaca(a) gaggcagctgagg
agcattttg(g) gaggctgagg
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tcttggtagtt(t) gagaccagcc
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gggggagggg(g) agggggaaggag
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| 7099 gggagcgcaa (a) gggagagtagt<br>7106 caaagggagaga (a) gtgccacat | 7128 gatotoatga (c) aactoocoo<br>7130 totoatgaca (a) ctoococao<br>7135 toacaactoo (c) coactatoa | 7136 gacaactece (c) cactateae 7137 acaactecee (c) actateaea | 7139 aacteceea (c) tateacaag<br>7144 ceecactate (a) caagaatag         | 7148 actatcacaa (g) aatagcatg<br>7149 ctatcacaag (a) atagcatgg    | 89628 cccagtcagg (a) aaatgccat atgatacatt (a) cagactataa | 89769 tggtggctta (c) agctgtaat gcattttggg (a) ggctgaggt            | 89865 aaccccatct (c) tyayac<br>89865 aaccccatct (c) tacaaa<br>0 6159 gaaaggaaaa (a) taaatc | 6180 gagccccaaaa (t) cactaagct ggccccaaaa (t) cactaagct 6209 aaqtqaaqct (d) qqaactqct | 0 6222 aactgettgg (g) gcaaactge<br>0 6234 caaactgeet (c) ctattttt   | o 6542 agcaccgtg (c) cctaccgcc<br>0 6542 ccaccgtgcc (c) taccgcctc<br>0 7029 ggtggaaggt (g) aaggggaag | 0 7057 gtottacaa (g) gtggcagga<br>0 totttacaag (g) tggcaggag      | 7085 gagagagaga (C) agagggagc<br>7086 agagagagac (a) gagggagcg<br>9agagagaca (g) agggagcgc |   | 7103 gcgcaaaggg (a) gaagtgcca<br>7104 cgcaaaggga (g) aagtgccac | 7131 ctcatgacaa (c) tcccccac<br>7142 tcccccacta (t) cacaagaa | Length 204228;  | 480 GGGGAGCGATCTCTGAAATCGCCCATTCAGTCCGACTTGGATGCGTTCCACTCGGGATTT 53    | 44987 GGGGAGCGATCTCAAATCGCCCATTCAGTCCGACTTGGATGCGTTCCACTCGG          | OY 540 CAAACATGCGCCAAAGAAGTCTTGCAATACCTCTCCGGTTTGAGAGCTGGACACCCAGG 599 | TTCTTGCCC 659  | 660 ACCCGCAGCTGTTGACTCAACAGGTCCTCTGAGGCAAAGGCACCGCGCGCTCCTCGG | 44807 ACCCGCAGCTCATCAACACTCCTCTCTGAGCAAAGGCACGCGCGCG                   | OY         720         GCCGGGTCCGCCCCCTGCCTGCCTGGCGCGGGCAGAAGCTGGAGCCCCTCGCC         779           DD         44747         GCCGGGCCGCCCCCTGCCTGCAGCGCGCGGGCAGAAGCTGGAGCCCCTCGCC         44688 | Oy         780         TACTGCGTGCCGTCATCCAGCGACTCAGCCCAGGCCCGAGGCTCGCCGAGAACGAC         839           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 840 ACGGACACCGACAGCGCTACGGCGGCGAAGCCGAGGCCGGACCGCAGAAAGGC 899           |

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BD176928

Novel bHLH type transcriptional gene, DEC2.

BD176928

BD176928.1 GI:30014187

JP 2002300878-A/1.

Homo sapiens (human)

SM Homo sapiens (human)

E ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 3274)

S Fujimoto, K., Shin, M. and Kato, Y.

Novel bHLH type transcriptional gene, DEC2

Patent: JP 2002300878-A 1 15-OCT-2002;

CHUGAI PHARMACEUT CO LTD

OS Homo sapiens (human)

PN JP 2002300878-A/1

PD 15-OCT-2002

PF 19-AUG-1999 JP 1999233286

PI KATSUMI FUJIMOTO, MEI SHIN, YUKIO KATO
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A61K45/00,
PC A61K48/00,A61P43/00,C12P21/08,C12N15/00,C12N5/00,A61K37/02
FH Key
FT CDS (135)..(1271).
Location/Qualifiers
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                                                      GATGTCTGACATGCTATTTTTGTAGGGAGAAAATATGTGCTAATGATATTTTGAGTTAAA
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| /organism="Homo sapiens"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:9606" | Query Match<br>Best Local Similarity 100.0%; Pred. No. 0;<br>Matches 2290; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Ay 1352 CGCCGCCGCCGCGTTCCCTGCCTGTCCTCGGTGTTGTCGCCCCTCCCGAGAAGGC 1411 | QY         1412         GGGCGCCGCGCGCGACCCTCCTGCCGCACGAGGTGGCGCCCCTTGGGGCGCCCCTTGGGCGCCGCACCC         1471           Db         1045         GGGCGCCGCGCGCGCGCCTCCTGCCGCACGAGGTGGCGCCCTTGGGGCGCCCCTTGGGCCCCCTTGGCGCCCCCTTGCCCCCTTGCCCCCTCCT | Oy         1472         CCAGCACCCGCACGCCCACCTACCTTCGCCGGGCCCCGCGAGCCGGGGAACCC         1531           Db         1105         CCAGCACCGCACGCACCCACCTGCCCTTCGCCGGGGAGCCCGGGGAACCC         1164 | SCTCCCTGAATCCTT<br> | Qy 1592 GTCCCGAAGGACGGAGGTTCAAGCAGTGAGAAGTTAAAATACCCTTAAGGAGGTTCAA 1651<br> | QY         1652         GCAGAGTGAAGTTAAAATACCCTTAAGGTCTTTAAGGGAAGTGTAATAGATGCAC         1711           Db         1285         GCAGAGTGAAGTTAAAATACCCTTAAGGTCTTTAAGGAAGTGTAATAGATGCAC         1344 | SAACAACAAAACAGGTGTTATGTGTACATTCGGAGTTCCTGTTTT 1 | OY 1772 GCTCATCCGCACCCCCCCCCCCCCCCCCCCCCCCCCCCC | Qy 1832 GTAAAGATCCTATGCGAAAGACACTGGCTCTTTTTTTAATCCCCCAAATAAAT | Qy 1892 CCCTTTTAGGCCATGTTCCATTATCTCTTAAATTGGAACCTAATTCGAGGAAGTAA 1951<br> | OY 1952 GAAGGGTCTGTGGCTGAGCTAGGTGAACCCCGGGGTAGGGGAAAGATGTTAACAC 2011<br> | QY 2012 CTTTGACGTCTTTGGAGTTGACATGGAACAGCAGGTAGTTGTTATGTAGAGCTAGTTCTC 2071<br> | QY 2072 AAAGCTGCCTGCTTTTAGGAGGCGTTCCACAAACAGATTGAGGCTCTTTTTAGAAT 2131 | OY 2132 TGAATTTACTCTTCAGTATTTTCTAATGTTCAGCTTTCTAAAGGCATATATTTTCAAA 2191<br> | Qy 2192 GAAGTGGATGCAGTTTCTCACGTTGCAACCTATTCTGAAGTGGTTTAAATGGTATCTC 2251 | actigcactcgttaaagaaacacggagctgggcca<br> |            |

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I sogai, T. and Yamamoto, J.

Direct Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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| Db         900 TCAATTAGTTTTAAGATATCTATAACTATAGGATACAAATCACTACAGTTCTCAGATTT 959           Qy         3493 ACACCTTTTTTTTTTTGTCATTGGCTTGATGTCACATCTCTTGCAAGCCTCCAG 3552           Db         960 ACAGCTTTTTTTTTTTTTTTTTTTTTTGCATTGCACATCTCTTGCAAGCCTCCAG 1019           Qy         3553 GCTCTGGCTTTGTCTACTGCTCGTTCCCAATGTATCTTAATGAAAAGTGCAAAAGAAAA 3612           Db         1020 GCTCTGGCTTTGTCTACCTGCTCGTTCCCAATGTATCTTAATGAAAAGTGCAAAAGAAAA 1079           Qy         3613 ACCTACCAATTAA 3625           Db         1080 ACCTACCAATTAA 1092 | DESTILT 9  10213166  10213166  10213166  1021316  1022316  102316  102316  102316  102316  103 |

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BV208394

BV208394

BHLHB3 2085 Rhesus macaque genomic DNA Macaca mulatta STS 01-JUL-2004

Clone MMA2085, sequence tagged site.

BV208394.1 GI:49533077

STS.

Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

E 1 (bases 1 to 797)

S Spindel, E.R., Pauley, M., Jia, Y., Boyle, N., Jiang, S., Gravett, C.,

Lupo, S.L., Ali, H., Ojeda, S.R. and Norgren, R.B.

Targeted amplification of the 3' end of rhesus macaque orthologs of human genes

L Unpublished (2004)
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                                        Bases 156-797 are 97% homologous (Blast) to bases 2596-3238 c
NM_030762.1. Primers were chosen to amplify genomic DNA in
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Division of Neuroscience
Oregon National Primate Research C6
505 NW 185th Avenue, Beaverton, OR
Tel: 403-690-5384
Email: spindele@ohsu.edu
Primer A: atgaattaatggactcatct
Primer B: actaaactttctaaaccagc
STS size: 797
PCR Profile:
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Submitted (18-OCT-1999) Lage H., Institute of Pa
University Berlin, University Hospital Charite,
D-10117 Berlin, GERMANY
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DSM-11"
/cell_line="MeWo"
/cell_type="melanoma"
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Homo sapiens partial unknovcells, 3'UTR, clone DMS-11 AJ270695
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ilarity 99.8%;
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region of BHLHB3. As human sequence was used to design the primers, the primer sequences are not included in the rhesus sequence provided below. To obtain additional information regarding primers or clones contact: Dr. Robert Norgren; Dept of Genetics, Cell Biology & Anatomy; University of Nebraska Medical Center; 986395 Nebraska Medical Center; Omaha, NE 68198. Email:
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/note="Organ: Liver; Vector: pGEM-TcDNA amplified from rhesus genomic forward and reverse primers listed
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Pred. No. 1.8e-211;
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/mol_type="genomic DNA"
/strain="Indian orgin"
/db_xref="taxon:9544"
/clone="MMA2085"
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Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 18023 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                                            for identification, cancer
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                                                            Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
Novel genes, compositions, kits, and methods f
assessment, prevention, and therapy of breast
Patent: WO 0151628-A 9175 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Pred. No. 1.4e-199;
0; Mismatches 0;
                                 Craniata, Ve
Catarrhini,
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/organism="Homo sapiens"
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Patent WO01
                                Chordata;
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Catarrhini; Hominidae;
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              Length 447;
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 30010 12-SEP-2002;
Chondrogene Inc. (CA)
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## ALIGNMENTS

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| 08<br>FION      | AI672308<br>ty63f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA_clone_IMAGE:2283773_3'<br>similar to contains_TAR1.t2 MSR1 MSR1 repetitive element ;, mRNA |
| NOI<br>NN<br>DS | <pre>sequence. AI672308 AI672308.1 GI:4852039 EST.</pre>   |
| NISM            | Homo sapiens (human)<br>Homo sapiens   |
|                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                       |
| NCE             |  |
| ជា្ម            | National Cancer Institute, Cancer Genome Anatomy Project (CGAP),<br>Tumor Gene Index   |
| NAL             | Unpublished (1997)<br>Contact: Robert Strausberg, Ph.D.  |
|                 | Email: cgapbs-r@mail.nih.gov<br>Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  |
|                 | Emmert-Buck, M.D., Ph.D.   |
|                 |  |
|                 | DNA Sequencing by: Washington University Genome Sequencing Center  |
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|                 | High quality sequence stop: 490.   |
| ES E            | Location/Qualifiers  |
| onrce           | /organism="Homo gapiens"   |
|                 | /mol_type="mRNA"   |
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|                 | prepared, and ss circles were made in vitro. Following HAP   |
|                 | purification, this DNA was used as tracer in a subtractive<br>hybridization reaction. The driver was PCR-amplified cDNAs                           |
|                 | from a pool of 5,000 clones made from the same library   |
|                 | (Clouelly 1322370-1323311, 1430007-143073, and M. 1500552-1502855). Subtraction by Bento Soares and M.   |
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stop: 635.

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                                                Indels
                             Length
                     DB 1; LC 5.1e-239; 0;
                                        ed. No. 5.
Mismatches
                            484; I
No. 5
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Pred.
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Fatima Bonaldo
                           ch 32.0%;
(1 Similarity 100.0%;
484; Conservative (
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Homo sapiens
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5539636"
/tissue_type="melanotic melanoma"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 619 Std Error: 0.00
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Pred. No. 4.3e-213;
0; Mismatches 0;
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:2405742 3'
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                                                      /Organism= now parterns
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2330737"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/clone_lib="Soares_NFL_T_GBC_S1"
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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wj45a04.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE: similar to TR: 035779 ENHANCER-OF-SPLIT AND HAIRY PROTEIN 1. ;, mRNA sequence.
A1819798
A1819798.1 GI: 5438877
EST.
Homo sapiens (human)
Homo sapiens (buman)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
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0
                                                 sapiens"
                451
primer: -40UP from Gibco

1 quality sequence stop: '

Location/Qualifiers

1..522
                                                 /organism="Homo/mol_type="mRNA"/db_xref="taxon:
                                                                                                                                                                                                                                                                                                                        0;
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Best Local Similarity 100.0%;
Matches 431; Conservative
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/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Lu19"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 557)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 340 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 441.
Location/Qualifiers

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                                                                                        (CGAP)
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/clone="IMAGE:2405742"
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differentiated (4 pooled tumors, including primary
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Pred. No. 5.1e-211;
0; Mismatches 0;
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Best Local Similarity 100.0%; F
Matches 430; Conservative 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2146370"
/lab_host="IMAGE:2146370"
/lab_host="DH108"
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/clone="Torgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same S libraries. The pools consisted of the following libraries and cloneIDs: Soares NbASF pool 1:
309384-310919, 323208-325895 Soares Nb2HF9 pool 1:
145032-147335, 147720-1488103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
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758280-760583, 772104-774407 Soares NbHPA pool 1:
758280-760583, 772104-774907, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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tj65c02.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clor
IMAGE:2146370 3' Similar to contains TAR1.t2 MSR1 repetitive
element ;, mRNA sequence.
A1459114
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Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 515)
S NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
L Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
Location/Qualifiers
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7g23f11.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:3307341
similar to TR:035779 COST79 ENHANCER-OF-SPLIT AND HAIRY-RELATED
PROTEIN 1. ;, mRNA sequence.
BE857082
BE857082.1 GI:10370753
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IMAGE:2556536 3'
HAIRY-RELATED
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 557)

S NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Fmail: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can b found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco

High quality sequence stop: 455.

Localion/Qualifiers
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                                              GCACAGATTAATAGAAAAGAAAAAAAGAGAG
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                        Indels
  Length
Score 380; DB 2; I
Pred. No. 4.2e-185;
); Mismatches 1;
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ch 25.1%;
il Similarity 99.8%;
430; Conservative
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wy97g05.x1 | similar to PROTEIN 1. AW073334 | AW073334.1 | EST.
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Query Match
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Matches 430
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os26c04.sl NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1606470 3' similar to TR:035779 C35779 ENHANCER-OF-SPLIT AND HAIRY-RELATED AA996006.1 GI:3182495
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 434)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                   Score 380; DB 2;
Pred. No. 4.2e-185;
0; Mismatches 1;
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ilarity 99.8%;
Conservative
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/tissue_type="blood"
/dev_stage="adult"
/dev_stage="adult"
/clone_lib="pBS-NE_Library"
/note="Vector: pBluescriptKS(+); Site_l: NotI; Site_2:
FCORV; Genomic DNA was digested with NotI and ECORV and
the resulting fragments were ligated into ZAPII/NotI
vector DNA. After the digestion with ECORV, the mixture
was run on o.8% LMP agarose gel, eluted a gel portion over
22 kb and purified with beta-agarase I. The purified DNA
was digested with NotI, run on 1% LMP agarose gel, and
eluted with Gel Extraction kit the DNA fragments ranging
0.7 to 4 kb, which cover on first-dimensional gel
comprising the central portion of the standard RLGS
profile. The DNA solution was ligated into pBluescript
KS(+) with NotI and ECORV ends. The ligated solution was
transformed into DH5a cell using electroporation machine."
Lee, K.T., Kim, J.H., Hahn, Y.S., Yang, J.O., Chu, M.Y., Kim, H.C., Oh, K.J., Kim, S.S., Yoo, H.S. and Kim, Y.S.
Rapid isolation of Noti-linked CpG island sequences from RLGS gel Unpublished (2003)
Contact: KIM YS
Human Genome Research Laboratory
Korea Research Institute of Bioscience and Biotechnology
S2 Ecoun-dong, Yuseong-gu, Daejeon 305-333, Republic of Korea Tel: 82-42-879-8119
Fax: 82-42-879-8119
Email: yongsung@kribb.re.kr
This result was produced by the program for Functional Analysis of Human Genome funded from Ministry of Science and Technology, Republic of Korea. Clones are available from the Center for Functional Analysis of Human Genome. See URL:
http://2lcgenome.kribb.re.kr/ for details or contact:
yongsung@kribb.re.kr.
Seq primer: T7 primer
Class: Not! site
High quality sequence stop: 310.
Location/Qualifiers
rce
High quality sequence stop: 310.
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Pred. No. 7.9e-149;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
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KRIBB 2D D67T7 pBS-NE Library Homo sapiens genomic clone KRIBB 2D D67 5, genomic survey sequence.

CG464925

CG464925.1 GI:35188360

GSS.

Homo sapiens (human)

Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                Ph.D.,
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           Tissue Procurement: Christopher Moskaluk, M.D., Ph.I Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Second Clone distribution: NCI-CGAP clone distribution infound through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 496 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 291.
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Pred. No. 4.8e-155;
0; Mismatches 0;
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il Similarity 100.0%; E
322; Conservative 0;
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                                                                                                       Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 301)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

L Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 317 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.

Location/Qualifiers
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ow54a11.s1 Soares parathyroid tumor NbHPA Homo sapiens
IMAGE:1650620 3' similar to TR:035779 035779 ENHANCER-C
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Pred. No. 3.7e-144;
0; Mismatches 0;
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/dev_stage="adult"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 299)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

L Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

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CDNA Library Preparation: M. Bento Soares, Ph.D.,

Email: cgapbs-r@mail.nih.gov

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LML at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 331 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.

Location/Qualifiers
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Ow51b10.x1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:1650331 3' similar to TR:035779 035779 ENHANCER-OF-SPLIT AND HAIRY-RELATED PROTEIN 1. ;, mRNA sequence.
AI028096.1 GI:3245405
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Pred. No. 4e-143;
0; Mismatches 0;
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleosto
Bukaryota; Metazoa, Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 451)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAF Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cond through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2359
Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                 GACTIGGATGCGTICCACTCGGGATTICAAACATGCGCCAAAGAAGTCTIGCAA
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ORGANISM
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AUTHORS
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BF432960
7n23all.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565341 3'
similar to contains_element TAR1 repetitive element ;, mRNA
sequence.
BF432960
BF432960.1 GI:11445123
EST.
                                        1403
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                                                   337
                CGGAGAGCTCTGCTCAGGAAGATCCCTCGCAGCAGGAAAGGAAGCTCCCTGAATCCTTG
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Pred. No. 8e-135
0; Mismatches
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Best Local Similarity 100.0%; I
Matches 283; Conservative 0;
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| QY         1356 ACGGCCGCACCTACCTGCCCTTCGCCGGGCCCCGCG                    | Qy         1416         CTCAGGAAGATCCCTCGCAGCCAGGAAAGGAAGCTC         | QY         1476 CGGAGGTTCAAGCAGAGTGAGAAGTTAAATACCCT   |  | LOCUS AA983880  SA9 DP MRN DEFINITION OP63c03.s1 Soares NFL T GBC S1 Homo sa IMAGE:1581508 3' Similar to TR:035779 HAIRY-RELATED PROTEIN 1. ;, mRNA seque | VERSION AA983880.1 GI:3162405 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens CRANISM Eukaryota; Metazoa; Chordata; Craniata | (bases 1 to 349)   NCI-CGAP http://www.ncbi.nlm.nih.gov/  National Cancer Institute, Cancer Gen Tumor Gene Index | COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov This clone is available royalty-free t IMAGE Consortium (info@image.llnl.gov)     | Insert Length: 612 Std Error: 0.0<br>Seg primer: -40m13 fwd. ET from Ame<br>High quality sequence stop: 348.<br>Location/Qualifiers | /organism="Homo sapiens"<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>/clone="IMAGE:1581508"<br>/lab_bost="DH108" | es NFJ<br>oled;<br>inker<br>plast<br>lung   | NCI_CGAP_GCB1) were mivited vitro. Following HAP_I tracer in a subtractives PCR-amplified cDNZ from the same 3 librali.A.G.E. clones 297.726408-728711, and 729.80ares and M. Fatima Exemples 1297.80ares and M. Fatima Exemples 100.800 from the same 3 libralines 297.800 from 100.800 17.3%; SCO   | 2 62  | Db 322 ACTCTGGGACATCTGGAGAAGCTGTAGTCTTGGAA AGCTGTAGTCTTGGAA AGCTGTAGTCTTGGAA AGCTGTAGTCTTGGAA AGCTGTAGTCTTGGAA AGCTGTAGTCTTGGAAA AGCTGTAACCGAGCAACAGCATCAGAAGATA AACCGAGCAACAGCATCAGAAGATA |   |
|---|--|---|--|---|--|--|--|---|--|---|--|--|---|--|---|
| OY 1229 GCCGCCGCCGCGTTCCCCTGCCTGTCTCGTGTTGTCGCCCCCTCCCGAGAAGGCGGGC 1288 | OY 1289 GCCGCCGCGCGCGCTCCTGCCGCACGTGGCGCCCCTTGGGGCGCCCCACCCCCAG 1348 | Qy         1349         CACCCGCACGCACCCACCTGCCCTTCGCCGGGCCCCGCGAGCCGGGAACCCGGAG         1408           Db         125         CACCCGCACGCACCCACCTGCCCTTCGCCGGGCCCCGGGAACCCGGAACCCGGAG         184 | OY 1409 AGCTCTGGTCAGGAAGATCCCTCGCAGCAAAGGAAAGCTCCCTGAATCCTTGCGTCC 1468 | Qy 1469 CGAAGGACGGAGGTTCAAGCAGAGTTAAAATACCCT 1511<br>   | RESULT 14<br>CR615693<br>LOCUS CR615693<br>DEFINITION full-length cDNA clone CS0DE013YK10 of Placenta of Homo sapiens                        | CR615693<br>CR615693.1 G1<br>HTC; CNSLT_CDN<br>HOMO Sapiens  | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhin 1 (bases 1 to 1109) Li,W.B., Gruber,C., Jessee,J. and Polay | cDNA libraries and normalizati<br>ng Liang Email : fliang@lifete<br>ength.invitrogen.com/ InVitroG                                  | ue<br>to 1109)<br>ssion<br>0-JUL-2004) Genoscope - Centre National de Sequencage :<br>EVRY cedex - FRANCE (E-mail : segref@denoscope ons fr      | genoscope.cns.fr)  Senoscope.cns.fr)  DNA was primed with a NotI-oligo(dT) primer. Five pri I, double-strand cDNA was digested with Not I and clon I and EcoR V sites of the pCMVSPORT 6 vector. Librar ed. Library was constructed by Life Technologies, a | <pre>ivision of Invitrogen. Location/Qualifiers 11109 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DE013YK10" /tissue_type="Placenta"</pre>  | /plasmid="pCMVSPORT_6" 10 28. 66000 276. np 2. 100000 1100 | Best Local Similarity 100.0%; Pred. No. 3.5e-131; Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0 | OY 1236 CCGCGTTCCCCTGCCTGTCTCGTGTTGTCCCCCCTCCCGAGAAGGCGGGCG  | Oy 1296 CCGCGACCTCTGCCGCACGAGGTGGCGCCCCTTGGGGCGCCGCACCCCCAGCACCCGC 1355 |

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GBC_S1"

Lor: pT7T3D-Pac (Pharmacia) with

Le_1: Not I; Site_2: Eco RI;

DNA from three normalized

L19W, testis NHT, and B-cell

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Fication, this DNA was used as

ybridization reaction. The driver

rom pools of 5,000 clones made

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302087, 682632-687239,

-731399. Subtraction by Bento
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hini; Hominidae; Homo.
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CGAGCCGGGGAACCCGGAGAGCTCTG
                                                 TCCCTGAATCCTTGCGTCCCGAAGGA
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        Qy
        362 TCTCTGAAATCGCCCATTCAGTCCGACTTGGATGCGTTCCACTCGGGATTTCAAACATGC 421

        Db
        202 TCTCTGAAATCGCCCATTCAGTCCGACTTGGATGCGTTCCACTCGGGATTTCAAACATGC 143

        Qy
        422 GCCAAAGAAGTCTTGCAATACCTCTCCCGGTTTGAGAGCTGGACACCCAGGGAGCCGCGG 481

        Db
        142 GCCAAAGAAGTCTTGCAATACCTCTCCCGGTTTGAGAGCTGGACACCCAGGGAGCCGCGG 83

        Qy
        482 TGTGTCCAGCTGATCAACACT 503

        Pb
        82 TGTGTCCAGCTGATCAACACT 61

        Db
        82 TGTGTCCAGCTGATCAACACT 61

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="melanotic melanoma"
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/note="Organ: skin; Vector bCMV-SPORT6; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life Technologies."
                  EB-2002
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                                                                               Homo Bapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcomi,
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 715)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies (ILNI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov.
Plate: LLAM1234 row: h column: 05
High quality sequence stop: 635.
S Location/Qualifiers
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                                                                                                Euteleostomi; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCCACAGATTATTGTACAGAGCCCCAAAATCGAAACAGAGGAAACGAACAGCAGTTG
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                   EST 20-FE IMAGE:55
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sapiens cDNA clone
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NIH_MGC_72
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100.0%; Pi
                                                           GI:18771584
                                                                             Homo sapiens (human)
                  BMS42244
AGENCOURT_6436506 1
5', mRNA sequence.
BM542244.1 GI:187
EST.
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                             DEFINITION
                                                                                        ORGANISM
                                                ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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RESULT 2
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AL542834 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE013YK10
5-PRIME, mRNA sequence.
AL542834
AL542834.3 GI:45718407
EST.
Homo sapiens (human)
SM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
EST.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ELi,W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30548385.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:645565"
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/clone_lib="NIH_MGC_101"
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XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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Homo sapieus

Homo sapieus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 892)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can I

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2634 row: k column: 17

High quality sequence stop: 684.

Location/Qualifiers

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//rranism="Homo sapiens"
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Mismatches 0;
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AGENCOURT_8732698 NIH_MGC_1(5', mRNA sequence.
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Library was not normalized."
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         division of Invitrogen.

This sequence belongs to sequence cluster 6711.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DE013BF05QP1&c=671

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="UI-H-EZ1-bca-h-10-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/tissue_type="Chondrosarcoma Grade II"
/tissue_type="Chondrosarcoma Grade II"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ch2"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ch2"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
ACT) He tail. The sequence tag for this library is
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                                                                                            Homo sapiens (human)

SM Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homoryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 665)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept.

Orthoapedics

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtain

from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this cDNA

sequence: 35-59, >AT_rich#Low_complexity (matched compliment)

Seg primer: M13 FORWARD

POLYA=YES.
                                                                                                                                                                            Euteleostomi
                                                                                                                                                                                                                                                                                                (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAATCACAAAGAAAGCTTTTTTAATAAGGCTTAAACCAAGACCTTGTCTAGATATTTT
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Pred. No. 1.5e-287;
0; Mismatches 0; Indel
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TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"
   sednence
 mRNA
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                                                           GI:21982874
 E21-bca-h-10-0-UI
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26-JUL-2002 A clone

EST

linear o sapiens

mRNA 1 Ch2 Homo

665 bp : NCI\_CGAP\_

BQ774398 UI-H-EZ1-bca-h-10-0-UI.81

RESULT 5 BQ774398/c LOCUS DEFINITION

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CA414694

T63 bp mRNA linear EST 07-NOV-2002
UI-H-EZO-bar-c-24-0-UI.s1 NCI CGAP_Ch1 Homo sapiens cDNA clone
UI-H-EZO-bar-c-24-0-UI 3', mRNA sequence.

MA414694.1 GI:24777345

RA714694.1 GI:24777345

BST.
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

I (bases 1 to 763)
Mational cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@aliowa.edu
The following repetitive elements were found in this cDNA
sequence: 189-213, AT rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
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TAAGTCAGGGAAGGAGATGGATGAGAAGGCCAGAATCATTCCTAGTACATTTGCTAACAC
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organism="Homo sapie:
mol_type="mRNA"
'db_xref="taxon:9606"
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GI:20400498
                                                           BQ219098
AGENCOURT 7575578 h
5', mRNA sequence.
BQ219098
BQ219098.1 GI:204(
EST.
Homo sapiens (humar
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Best Local Similarity
Matches 573; Conser
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                                                                                                                                 ORGANISM
                                                                      DEFINITION
                                        BO219098/c
LOCUS
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VERSION
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/clone="UI-H-EZO-bar-c-24-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/loote="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP Ch1 is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
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                                                                                                                                                                                                                                           Length 763
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                TGATCACGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ0
TAG_SEQ=ATCTAATATG"
                                                                                                                                                                                                                                          Score 595; DB 6; I
Pred. No. 9.9e-273;
); Mismatches 0;
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0
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Best Local Similarity 99.9%;
Matches 715; Conservative
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Homo sapiens (human)

Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 964)

In (bases 1 to 964)

In (bases 1 to 964)

In (bases 1 to 964)

In (bases 1 to 964)

In (bases 1 to 964)

In (bases 2 trausberg, Ph.D. (base)

Contact: Robert Strausberg, Ph.D. (base)

Email: Gapbys-rômmal.nih.gov

Tissue Procurement: ATCC/CTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MGC clone distribution information can be found through the I. M.A.G.B. Consortium/LiNL at:

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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A1819798

N wj45a04.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2405742 3'
similar to TR:035779 ENHANCER-OF-SPLIT AND HAIRY-RELATED
ROTEIN 1. ;, mRNA sequence.

N A1819798
A1819798.1 GI:5438877
EST.
Homo sapiens (human)
SM Homo sapiens (human)
SM Homo sapiens (human)
SM Homo sapiens (human)
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SM Homo sapiens (human)
SM Homo sapiens (human)
SM Homo sapiens (human)
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

SM Homo sapiens (human)
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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|CCTTAAATTATTTTAAAAAAT
                                                                           0;
                                     Query Match
Best Local Similarity 99.9%;
Matches 681; Conservative
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 786)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 28-52, AT rich#Low_complexity (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EU1-bad-k-13-0-UI"
/tissue_type="Madult"
/dev_stage="Adult"
/dev_stage="Adult"
/lone_lib="NCI CGAP_Ct1"
/clone_lib="NCI CGAP_Ct1"
/clone_lib="NCI CGAP_Ct1"
/note="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR I; Site_2: Not I;
NCI CGAP_Ct1 is a normalized cDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                      3182
                                                                                                                                                                                                                                                                                                                                                          29-MAY-2002
clone
                                                                                              154
TTGGTACA
                                                                                                                                                                                                                                                                                                                                                          EST 2
                                                                                                                                  TCTTTTGGGGAGGATTTGCTGAAAGTTGCACTTTTGTTACAATGCTTATGC
  A linear
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      BQ447103
UI-H-EU1-bad-k-13-0-UI.S1 NCI CGAP Ct1 Hc
UI-H-EU1-bad-k-13-0-UI 3', mRNA sequence.
BQ447103
BQ447103.1 GI:21250215
EST.
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TGATCACGCT.
TAG_TISSUB=ost
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COMMENT

TAG\_LIB=UI-H-EU1 TAG\_SEQ=TGATCACGCT

Length

2593 2893 ï 2713 2833 2953 3013 3073 3193 2773 475 415 355 594 295 235 115 534 175 ACAACAAAAAACCAAACTGATATATCCTATATTCTGTTAAAATTCAAAAGTGAAC ATCACAAAGAAAGCTTTTTTAATAAGGCTTAAAACCAAGACCTTGTCTAGATATTTTTAGT TGTTGCCAAGGTAGCACTGTGAGAATCTCACTTGGATGTTATGTAAGGGGTGAGACAC ATCACAAAGAAAGCTTTTTAATAAGGCTTAAAACCAAGACCTTGTCTAGATATTTTAGT Gaps .. H Indels 56; 56; 0; Score 561; DB 5 Pred. No. 1.8e-2; ; Mismatches CTGTAAAAAAGTGCACTGAA 3215

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 720)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries

D Osteoarthritic Sartilage cDNA libraries

E 21482651

Contact: Sanjay Kumar
                                                                                                                                                                      cartilage) Homo sapiens cDNA, mRNA
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           CAGCTGATCAACCACTTGCACGCCGTGGCCACCCCAGTTCTTGCCCACCCCGCAGCTGTTG
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GlaxoSmithKline
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia,
Tel: 610-270-7245
Fax: 610-270-7245
Email: sanjay kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
1. .720
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/tissue type="cartilage"
/lab host="E.coli DH10 B"
/clone lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_
Directional"
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Pred. No. 4.5e-254; ); Mismatches 1;
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Best Local Similarity 99.8%;
Matches 606; Conservative
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                                                                                                                                                                                                                                                         sapiens (human)
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Eukaryota; Mammalia; E
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                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone lib="NCI CGAP_Lu19"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
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1 can be
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/ organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="IMAGE:2405742"

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metastatic)"
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                                                           Ph.D.,
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Second Clone distribution: NCI-CGAP clone distribution inffound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 340 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 441.
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Matches 556; Conservative 0;
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mRNA sequence.
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Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 630)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (M
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov

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Length

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Score 554; DB 4; Pred. No. 4.1e-20; Mismatches

Query Match Best Local Similarity 100.0%; Matches 554; Conservative 0

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 523)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

L Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 490.
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                              s cDNA clone IMAGE:2283773 repetitive element ;, mRNA
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UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (ENI and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
bento-soares@ulowa.edu
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
TAG_LIB=UI-CF-FN0
TAG_LIB=UI-CF-FN0
TAG_SEQ=CTGCTCAGGT"
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Genetics (www.resgen.com) or from Open Biosyst
(www.openbiosystems.com).
The following repetitive elements were found
sequence: 189-213, >AT_rich#Low_complexity (ma
Seq primer: M13 FORWARD
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Pred. No. 6e-246;
0; Mismatches 0;
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late: LLAM10003 row: b column: 13
lgh quality sequence stop: 638.
Location/Qualifiers
1. 955
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4361004"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 84"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 955)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10003 row: b column: 13
High quality sequence stop: 638.
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602273249F1 NIH_MGC_84 Homo simRNA sequence.
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(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

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2004, 19:33:10 ; Search time 196 Seconds (without alignments) 1420.823 Million cell updates/sec

US-10-078-650-12 2517 1 MDEGIPHLQERQLLEHRDFI.....PGNPESSAQEDPSQPGKEA Title: Perfect score: Sequence:

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BLOSUM62 Gapop 10.0 , Gapext Scoring table:

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1825181 seqs, 575374646 residues Searched:

1825181 hits satisfying chosen parameters: of Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% . Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

## SUMMARIES

| cription            | 9c0j9 homo sa | Stat1 homo sapi | 7yqc9 canis fam | 99pv5 mus muscu | ad18970 mus mus | 35779 rattus no | 8cgh4 mus mu | 185 mus muscu | ac33281 mus      | ac41056 mus | 6ny50 brachy | ah66738 brachyd | 35780 rattus | 76jq4 rattus    | ad01588 rattus | 14503 homo sapie | ag33202 homo sap | egne9 xenopu | 7qjd2 anopheles       | 9u450 drosophila | 9vgz5 drosophi | 8cd44 mus muscu | 9qus4 mus muscul | Baxv6 brac | 911j1 chla | 7t5d9 cercopithe | 9gzf7 caenor | 7t591 cercopithe | 9ubp5 homo sapie | xu8 caenorhab | 9bit7 nephila in |
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| 0 gallus | ap44728 gallus g      | xlp9 gallus    | ap44729 gallus g | jj70 strongyloc | as46235 strongyl | 9h7s9 homo sapie | 6v6z4 branchi | aq93669 br | 919    | 9ng87 homo sa | vj16 drosophil | 9nfw8 cupie |            |
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| OEXTOO   | AAP44728              | Q6XLP9         | AAP44729         | Q6JJ70          | AAS46235         | Q9H7S9           | Q6V6Z4        | AAQ93669   | 076160 | Q9NQ87        | 76             | Q9NFW8      | HES1_CHICK |
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Q8TAT1;
Q8TAT1;
Q8TAT1;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Basic helix-loop-helix domain containing, class B, 3.
Name=BHLHB3;
Homo sapiens (Human).
Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Eukarvota; Metazoa; Chordata; Craniata; Hominidae; Mommalia; Eutheria; Primates; Catarrhini; Hominidae; MCBI_TaxID=9606;
                                                                                                                                                                             1; Repressor; Transcriptic
Basic motif.
Helix-loop-helix motif.
Orange.
Ala/Gly-rich.
4; 2BECDC2FDEB7CE14 GRC64
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GO; GO:0003700; F:transcription factor activity;
GO; GO:0030154; P:cell differentiation; NAS.
GO; GO:0008283; P:cell proliferation; NAS.
GO; GO:0009887; P:organogenesis; NAS.
GO; GO:0006355; P:regulation of transcription, DN InterPro; IPR001092; HLH_basic.
InterPro; IPR001092; HLH_basic.
Pfam; PF07527; Hairy_orange.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
DNA-binding; Nuclear protein; Repressor; Transcription DNA_BIND
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     activity;
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Pred. No. 7.4e-122
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Local Similarity 99.6%;
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ESQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUB=21388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

RISCULE PLO. Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marushan K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Green E.J., Lu X., Gibbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Marra M.A., Schmutz J., Myers R.M., Butkerfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butkerfield Y.S.,

A Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human and more cDNA sequences."
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TISSUE=Placenta;
Strausberg R.;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC025968; AAH25968.1; -.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
R InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
R SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
R PROSITE; PS50888; HLH; 1.
SEQUENCE 482 AA; 50525 MW; 23EBD420C6B0CE03 CRC64;
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d. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1.2e-121;
); Mismatches 1;
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PIR; JC7584; JC7584.
MGD; MGI:1930704; Bhlhb3.
InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
SMART; SM00353; HLH; 1.
DNA-Linding; Nuclear protein; Rel DNA-Linding; Nuclear protein; Rel DOMAIN 129 175 Oran BOMAIN 321 373 Ala, SEQUENCE 410 AA; 43946 MW; 41
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Canis
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Last sequence update)
Last annotation update)
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ia; Canidae;
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Name=SHARP1;
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae
NCBI_TaxID=9615;
[1]
SEQUENCE FROM N.A.
TISSUE=Retina;
MEDLINE=22791403; PubMed=12909371;
Kukekova A.V., Aquirre G.D., Acland G.M.;
"Cloning and characterization of canine SHARP1 and positional candidate for canine early retinal dege Gene 312:335-343(2003).
EMBL; AY204567; AAP12464.1; -.
EMBL; AY204568; AAP12464.1; -.
EMBL; AY204567; AAP12465.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:000355; P:regulation of transcription, DN; InterPro; IPR001092; HLH basic.
InterPro; IPR001092; HLH basic.
InterPro; IPR001092; HLH basic.
Ffam; PF07527; Hairy_orange; 1.
PFam; PF07527; Hairy_orange; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
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Best Local Similarity 90.3%;
Matches 465; Conservative
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01-OCT-2003 (
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21092582; PubMed=11162494; DOI=10.1006/bbrc.2000.4133;

Minimoto K., Shen M., Noshiro M., Matsubara K., Shingu S., Honda K., Yoshida E., Suardita K., Matsuda Y., Kato Y.;

Molecular cloning and characterization of DEC2, a new member of bas I helix-loop-helix proteins.";

Elochem. Blophys. Res. Commun. 280:164-171(2001).

-!- FUNCTION: May be a transcriptional repressor that represses both basal and activated transcription.

-!- FUNCTION: May be a transcription.

-!- SUBUNIT: Homodimerize.

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

-!- TISSUE SPECIFICITY: Expressed in skeletal muscle, brain and lung C. -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

-!- SIMILARITY: Contains 1 orange domain.
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Basic motif.
Helix-loop-helix motif.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Ala/Gly-rich.
40A87281B08E233D CRC64;
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Q99PV5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Class B basic helix-loop-helix protein 3 (bHLHB3)
expressed in chondrocytes protein 2) (mDEC2).
Name=Bhlhb3; Synonyms=Dec2;
Mus musculus (Mouse).
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Pred. No. 3.9e-77;
1; Mismatches 37;
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h 64.9%;
Similarity 72.0%;
50; Conservative
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PubMed=11162494;
Fujimoto K., Shen M., Noshiro M., Matsubara K., Shingu Yoshida E., Suardita K., Matsuda Y., Kato Y.;
"Molecular cloning and characterization of DEC2, a new helix-loop-helix proteins.";
Biochem. Biophys. Res. Commun. 280:164-171(2001).
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S., Honma K.,
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Hamaguchi H., Fujimoto K., Kawamoto T.,
Takeda N., Nagai R., Furukawa M., Honma
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LLTPQVPSGRGSGRAPCSAGAAASGPER
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PubMed=12397359;
Honma S., Kawamoto T., Takagi Y.,
Kato Y., Honma K.;
"Decl and Dec2 are regulators of t
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Eukaryota; Metazoa; Chordata; Cr Mammalia; Eutheria; Rodentia; Schords NCBI_TaxID=10090;
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Sciurognathi; Muridae; Murinae; Rattus
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and hairy-related proteins
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STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
MEDLINE=98193761; PubMed=9532582;
Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;
Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;
Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;
Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;
"SHARPs: mammalian enhancer-of-split- and hairy-related pr
coupled to neuronal stimulation.";
Mol. Cell. Neurosci. 10:460-475(1997).
-!- FUNCTION: May be a transcriptional repressor that repr
basal and activated transcription.
-!- FUNCTION: Modimerize.
-!- SUBUNIT: Homodimerize.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Highly expressed in subregions of moderately expressed in skeletal muscle, heart. Weakly
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B3_RAT STANDARD; PRT; 410 AA.
BHB3_RAT STANDARD; PRT; 410 AA.
035779;
28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
class B basic helix-loop-helix protein 3 (bHLE)
and hairy-related protein 1) (SHARP-1).
Name=Bhlhb3; Synonyms=Sharp1;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertek
Mammalia; Eutheria; Rodentia; Sciurognathi; Mu
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SIMILARITY: Contains 1 basic helix-loop-he
SIMILARITY: Contains 1 orange domain.
CAUTION: Ref.1 sequence differs from that
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Score 1634; D. Pred. No. 3.9e
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                                                                                                                                                                                                                                                                                                                                                                                     GGPGGGA
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                                    tions
in
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            This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 SLKSPIQSDLDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVAT
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAALIGPDPAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAPFCLP
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                                                                                                                                                                                                                                                                                          410;
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                                                                                                                                                                                                                    Length
                                                                                                                                                           Transcription
                                                                                                                                                                                                    CRC64
                                                                                                                                                        1; Repressor; Transcriptic
Basic motif.
Helix-loop-helix motif.
Orange.
Ala/Gly-rich.
4; 829705CA3A013127 CRC64
                                                                                                                                                                                                                  Score 1624; DB 1;
Pred. No. 1.3e-76;
3; Mismatches 37;
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                                                                                  FRAME
                                                                            EMBL; AF009329; AAB63586.1; ALT_FR

RGD; 70900; Bhlhb3.

InterPro; IPR001092; HLH basic.

InterPro; IPR003650; Orange.

Pfam; PF07527; Hairy orange; 1.

Pfam; PF00010; HLH; 1.

SMART; SM00353; HLH; 1.

SMART; SM00511; ORANGE; 1.

PROSITE; PS50888; HLH; 1.

DNA-binding; Nuclear protein; Repring bona BIND 45 57 Basic DOMAIN 58 100 Helix DOMAIN 321 344 Ala/G. SEQUENCE 410 AA; 43917 MW; 829
 249
                                                                                                                                                                                                                                  23;
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position
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PAKDAP
frameshift
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QBCGH4;
01-MAR-2003
01-MAR-2003
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TISSUE=Mammary gland;

X SEQUENCE FROM N.A.

TISSUE=Mammary gland;

X Relaiser R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riasher R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buendow M.F., Casavant T.L., Scheetz T.E.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Schmutz J., Myers R.M., Butterfield Y.S.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human and more and an analysis of more than 15,000 full-length human and mannare H.
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TISSUE=Mammary gland;

A Strausberg R.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; BC037742; AAH37742.1; -..

RMGD; MGI:1930704; Bhlhb3.

RGO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA InterPro; IPR001092; HLH basic.

R InterPro; IPR003650; Orange.

R InterPro; IPR003650; Orange.

R Pfam; PF07527; Hairy orange; 1.

R SMART; SM00353; HLH; 1.

SMART; SM00511; ORANGE; 1.

R SMART; SM00511; ORANGE; 1.

R PROSITE; PS50888; HLH; 1.

SMART; SM00511; ORANGE; 1.

SMART; SM00511; ORANGE; 1.

SMART; SM00511; ORANGE; 1.
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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.. Acad. Sci. U.S.A. 99:16899-16903(2002).
        update)
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Pred. No. 1.1e-39;
); Mismatches 5;
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LLTPQVPSGRGSGRAPCSAGA
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01-MAR-2004 (TrEMBLrel. 2
Bhlhb3 protein (Fragment)
Name=Bhlhb3;
Mus musculus (Mouse).
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RESULT 8 BHB2\_MOUSE

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TISSUE=Mammary gland;

MEDITAR=22388237; Pubmed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Alscella S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Blat N.K.,

Alschild S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Blat N.K.,

Alschild S.F., Jordan H., Moore T., Wax S.I., Wang U., Hsieh F.,

Diatchenko L., Marusina K., Faramer A.A., Rubin G.M., Hong L.,

Blatchenko L., Marusina K., Faramer A.A., Rubin G.M., Hong L.,

Brahe S.S., Logellanon N.A., Peters G.J., Abramon R.H., Scheetz T.B.,

Brahe S.S., Logellanon N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

Broak S.A., McEwan P.J., McKernan K.J., Madek J.A., Mulyk S.W.,

Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

Brake J., Helton E., Setteman M., Madan A., Rodrigues S., Sanchez A.,

Rahey J., Helton E., Young A.C., Shevchenko Y., Solbbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Schain J.E., Jones S.J.M., Marza M.A.,

Rodriguez A.C., Grimwood J.S., Jones S.J.M., Marza M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

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"Generation and initial analysis of more than 15,000 full-length human

"Genera
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97203270; PubMed=9050988; DOI=10.1038/sj.onc.1200912; Dear T.N., Hainzl T., Follo M., Nehls M., Wilmore H., Matena K.
                                                                                                                               (Stimulated
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chambon P.;
"Overexpression of Stral3, a novel retinoic acid-inducible "Overexpression of Stral3, inhibits mesodermal and prom basic helix-loop-helix family, inhibits mesodermal and prom neuronal differentiation of P19 cells.";
Genes Dev. 11:2052-2065(1997).
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u
                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Class B basic helix-loop-helix protein 2 (bHLHB2)
retinoic acid 13) (E47 interaction protein 1) (ei)
Name=Bhlhb2; Synonyms=Stra13, Clast5;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND INTERACTION WITH E47/TCF3 STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bouillet
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S
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Embryonic carcinoma;
MEDLINE=97427857; PubMed=9284045;
Boudjelal M., Taneja R., Matsubara
     PRT;
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5; TISSUE=Spleen;
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Oncogene 14:891-898(1997)
        STANDARD;
        BHB2 MOUSE STAN
035185; P97289;
28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
05-JUL-2004 (Rel. 4
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STRAIN=C57BL/6; T
O-Wang J.;
"Isolation of a C
Submitted (MAR-20
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expressed in developing muscle.
INDUCTION: Stimulated by retinoic acid (RA).
SIMILARITY: Contains 1 basic helix-loop-helix
SIMILARITY: Contains 1 orange domain.
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AC BAC33281

DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)

DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)

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DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)

DE 16 days embryo head cDNA, RIKEN full-length enriched library,

DE clone:C130042M06 product:basic helix-loop-helix domain containing,

DE class BC, full insert sequence.

OS Mus musculus (Mouse).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

OX NCBI_TaxID=10090;
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STRAIN=C57BL/6J; TISSUE=Head;

MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Head;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Katoh H., Kawai J., Kojima Y., Ondo S., Konno H., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tag
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annot
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phe
"Analysis of the mouse transcriptome based on f
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse c
Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cl
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Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK048242; BAC33281.1; -. B392893CD49292BC CRC64;
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14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Male submandibular gland CRL-1734 SCA-9 clone 15 cDNA, RII full-length enriched library, clone:G430067G17 product:bashelix-loop-helix domain containing, class B2, full insert
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Sciurognathi; Muridae;
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STRAIN=Swiss Webster; TISSUE=Submandibular gland;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I andlysis of the mouse transcriptome based on function 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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SEQUENCE FROM N.A.
STRAIN=Swiss Webster; TISSUE=Submandibula
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length
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Eukaryota; Metazoa; Chordata,
Mammalia; Eutheria; Rodentia,
NCBI_TaxID=10090;
                                                                         Query Match
Best Local Similarity 43.1%;
Matches 184; Conservative
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TISSUE=Kidney;
Strausberg R.;
Submitted (MAR-2004) to
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

A Fukuda K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hoyashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Rouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Ohsato N., Okazaki Y.,

A Kurihara C., Matsuyama T., Miyazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Taqami M.

A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO90032; BAC41056.1; -.

EMBL, AKO90032; BAC41056.1; -.
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P. Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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STRAIN=Swiss Webster; TISSUE=Submandibular gland;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
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Pred. No. 6e-28;
5; Mismatches 102;
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                                 STRAIN=Swiss Webster; TISSUE=Submandibular MEDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning." Meth. Enzymol. 303:19-44(1999).
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409:685-690(2001)
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SEQUENCE FROM N.A.

TISSUE=Kidney;

X TISSUE=Kidney;

X TABUSDE=22388257; PubMed=12477932;

X Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,

B Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay E.J., Mulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hakesley R.W., Touchman J.W., Madan A., Rodrigues S., Sanchez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

A Jones S.J., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:76913.
Name=zgc:76913;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                       -LEKCWYPTSV----PVLYPGLNTSAAA
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d. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 6.6e-28;
3; Mismatches 122;
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InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
Hypothetical protein.
SEQUENCE 403 AA; 44682 MW; 08
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databases

EMBL/GenBank/DDBJ

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180
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SEQUENCE FROM N.A.

TISSUE-2138825; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H.; Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H.; Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H.; Moore T., Max S.I., Wang J., Hsieh F.,

RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abamson R.D., Mullahy S.J.,

RA Raha S.W., McEman P.J., McKernan K.J., Malek J.A., Gunnaratue P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Fulyk S.W.,

RA Fichards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

RA Faley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Faley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Mority M., Mara M.J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RGeneration and initial analysis of more than 15,000 full-length huma

RT "Generation and initial analysis of more than 15,000 full-length huma

RT "And mouse cDNA sequences.";
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В. Ж.,
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:76913.
ZGC:76913.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto: Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinifo
PCMSKHPSLDISDMQGMDF-PMYVYKPRRGMKRSEDSK--DTYKLPHRLIEKU
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                           CIAQLKDLLPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIJALQI
                                             SLKSPIQSDLDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVA
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Sciurognathi; Muridae; Murinae; Ra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BHB2 RAT STANDARD; PRT; 411 AA. 035780; 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2004 (Rel. 44, Last annotation update) 05-JUL-2004 (Rel. 44, Last annotation update) class B basic helix-loop-helix protein 2 (bHLHB2) and hairy-related protein 2) (SHARP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLTQQVPLSKGTGAPSAAGSAAAPCLERAGQK---LEPLA
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SUBCELLULAR LOCATION: Nuclear (By similarity)
TISSUE SPECIFICITY: Expressed in heart, brain,
liver, muscle, kidney, uterus and gut.
SIMILARITY: Contains 1 basic helix-loop-helix
SIMILARITY: Contains 1 orange domain.
                                                                                                               Score 684.5; DB 2;
Pred. No. 6.6e-28;
; Mismatches 122;
                                                                       42DC03FFF298E
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MEDLINE=98193761; PubMed=9532582;
Rossner M.J., Doerr J., Gass P., Schwab M.H., NansHARPs: mammalian enhancer-of-split- and hairy-coupled to neuronal stimulation.";
Mol. Cell. Neurosci. 10:460-475(1997).
-!- FUNCTION: May function as a transcriptional differentiation.
-!- SUBUNIT: Able to homodimerize or heterodimer
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
Submitted (MAR-2004) to the EMBL; BC066738; AAH66738.1; Hypothetical protein. SEQUENCE 403 AA; 44682 MV
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40.1%;
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186, Conservative
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SEQUENCE FROM N.A.
TISSUE=Kidney;
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                      This SWISS-PROT entry is copyright, It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstatio the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch).
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Q76JQ4;
Q76JQ4;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
8-JUL-2004                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - СЅРГІСРИРНОРР
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Helix-loop-helix motif.
Orange.
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186; Conservative 45; Mismatches 100;
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RGD; 68439; Bhlhb2.
InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy Orange; 1.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
DNA-binding; Nuclear protein; Tre
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BAD01588;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Enhancer of split-and hairy-related protein-2.
SHARP-2.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                           gene: hepatic
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                                                                          Mizutani
                                                                                                                                                                                                                                                                                                                                                            Score 679.5; DB 2;
Pred. No. 1.2e-27;
5; Mismatches 103;
[1]
SEQUENCE FROM N.A.
TISSUE=Kidney;
PubMed=14725860;
Hirano S., Yamada K., Kawata H., Shou Z., Mizutai Mayumi M., Miyamoto K.;
"The rat enhancer of split- and hairy-related preexpression, genomic structure, and promoter analy Arch. Biochem. Biophys. 422:81-90(2004).
EMBL; AB096137; BAD01588.1; -.
InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF07527; Hairy orange; 1.
Pfam; PF07527; Hairy orange; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
SRQUENCE 411 AA; 45557 MW; 2086DABB3DB82058
                                                                                                                                                                                                                                                                                                                         2086DABB3DB82058
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Local Similarity 43.1%;
Les 184; Conservative 45
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192
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                                                                                                                                   hepatic
     Shigematsu Y.,
                                                                                                                    Gaps
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                                                                                             411;
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Hirano S., Yamada K., Kawata H., Shou Z., Mizutani T., & Mayumi M., Miyamoto K.;
"The rat enhancer of split- and hairy-related protein-2 expression, genomic structure, and promoter analysis."; Arch. Biochem. Biophys. 422:81-90(2004).
EMBL; AB096137; BAD01588:1; -. SEQUENCE 411 AA; 45557 MW; 2086DABB3DB82058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    --PLLYPGLNTSAAA
                                                                                        Query Match

27.0%; Score 679.5; DB 2;
Best Local Similarity 43.1%; Pred. No. 1.2e-27;
Matches 184; Conservative 45; Mismatches 103;
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ime : 200 secs
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5.1.6 Compugen Ltd version - 2004 GenCore (c) 1993 Copyright

using sw model protein search, OM protein

Run

20:05:13 2004, December on:

; Search time 40 Seconds (without alignments) 1164.223 Million cell updates/sec

Title: Perfect

484 ې۵ ..PGNPESSAQEDPSQPGKEA US-10-078-650-12 484 1 MDEGIPHLOERQLLEHRDFI score: Sequence

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 segs, 96216763 residues Searched:

0 Word size

283416 hits satisfying chosen parameters: ö number Total

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Listing first 45 summaries

Database

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ve a printed, Pred. No. is the number of results predicted by chance to hav score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

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| SUMMARIES | 1              | C758             | C758             | C554 | 5703             | C527            | 5366            | 831223         | 4823          | 0261           | 5603           | 1635      | 1374      | C595         | 4842         | 1491            | 3823         | <b>C755</b> | 1369  | 1323   | 1323 | 1322  | 1323  | 5501    | 5718        | 3132          | 1254          | 4356         | 0240          | 4818           |
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|           | Score          | 440              | 81               | 52   | 16               | 16              | 16              | 16             | 16            | 16             | <del>1</del> € | 76        | 9<br>T    | 15           | 15           | 15              | 15           | 15          | 15    | 15     | 15   | 12    | 15    | 15      | 15          | 15            | 14            | 14           | 4             | 14             |
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| probable homeobox<br>probable homeobox<br>zinc finger protei | omeotic protein<br>rotein H05C05.1<br>palt protein - f | elated to PAN2 p<br>emale sterile ho<br>robable MASH-2 p | chaete scute<br>omeotic prote<br>inc-finger pr | egmentation prot<br>asic helix-loop- | zinc-finger protei<br>myc-associated zin |
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helix-loc Yoshida, basic ×, of Honda, member .; .; RESULT 1
JC7583

basic helix-loop-helix protein, DEC2 - human
C; Species: Homo sapiens (man)
C; Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change
C; Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change
C; Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change
C; Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change
C; Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change
C; Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.
Biochem. Biophys. Res. Commun. 280, 164-171, 2001
A; Reference number: JC7583; MUID:21092582; PMID:11162494
A; Reference number: JC7583
A; Molecule type: mRNA
A; Residues: 1-482 < FUJ>
A; Molecule type: mRNA
A; Residues: 1-482 < FUJ>
A; Molecule type: mRNA
A; Residues: JC7583
A; MOLOSIS - This protein, a novel member of the DEC subfamily of C; Genetics:
A; Gene: dec2
A; Map position: 12p11.23-p12.1
C; Keywords: transcription factor
C; Keywords: transcription factor
F; J130-173/Domain: Orange #status predicted
F; J30-173/Domain: Orange #status predicted
F; J30-173/Domain: Orange #status predicted change new

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basic helix-loop-helix

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Gaps ·. 482; Indels Length ·; 2 DB Score 440; DB Pred. No. 0; 0; Mismatches 0; Query Match Best Local Similarity 100.0%; Matches 440; Conservative

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104 102 164 162 DTYKLPHRLIEKKRRDRINECIAQLKDLLPEHLKLTTLGHLEKAVVLELTLKHLKALTAL 43 45 105 103 a B a ð ठ

282 344 DSRGGGGGGGGGAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGGAPFPQPAA 225 223 285  $\delta$ g  $\delta$ 

464

AAAAAAAFPCLSSVLSPPPEKAGAAATLLPHEVAPLGAPHPQHPHGRTHLPFAGPRE

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RESULT 6
A53662
homeotic protein HB9 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C;Accession: A53662
R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J, Biol. Chem. 269, 19968-19975, 1994
A;Title: A novel human homeobox gene distantly related to proboscipedia is expressed in A;Teference number: A53662; MUID:94327547; PMID:7914194
A;Reference number: A53662
A;Accession: A53662
A;Accession: A53662
A;Kesidues: 1-403 <+ARR>
A;Residues: 1-403 <+ARR>
A;Residues: 1-403 <+ARR>
A;Cross-references: GB:U07663
A;Note: the nucleotide sequence and conceptual translation as given are self-consistent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:BAA11555.1
                                                                                             Potter,
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C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_ch
C;Accession: 157039
R;Hsieh-Li, H.M.; Witte, D.P.; Szucsik, J.C.; Weinstein, M. Mech. Dev. 50, 177-186, 1995
A;Title: Gsh-2, a murine homeobox gene expressed in the dev
A;Title: Gsh-2, a murine homeobox gene expressed in the dev
A;Reference number: 157039; MUID:95344993; PMID:7619729
A;Reference number: 157039; MUID:95344993; PMID:7619729
A;Residues: 1-303
A;Residues: 1-305 <RES>
A;Cross-references: GB:S79041; NID:g1042008; PIDN:AAB34947
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the compan
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Pred. No. 2.9e-06;
); Mismatches 0;
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2.8e-06;
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Matches 16; Conservative
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Best Local Similarity 100
Matches 16; Conservative
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C; Species: Homo sapiens (man)
C; Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Ju
C; Accession: JC5547
R; Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyand
B; Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyand
B; Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyand
B; Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyand
B; Resorem Biophys. Res. Commun. 236, 294-298, 1997
A; Reference number: JC5547; MUID: 97382424; PMID: 9240428
A; Reference number: JC5547
A; Molecule type: mRNA
A; Residues: 1-412 <SHE>
A; Residues: UNIPROT: 014503; DDBJ: AB004066; NID: 92308996; PIDN
C; Comment: This protein is involved in the control of cell different: F; 51-108/Region: helix-loop-helix #status predicted
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JC7584
basic helix-loop-helix protein, DEC2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Shen Biophys. Res. Commun. 280, 164-171, 2001
A;Title: Molecular cloning and characterization of DEC2, a new m A;Reference number: JC7584
A;Reference number: JC7584
A;Accession: JC7584
A;Accession: JC7584
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Pred. No. 2.9e-64;
0; Mismatches 0;
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Similarity 100.0%;
81; Conservative C
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157039
genomic screen homeobox protein
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Matches 52; Conser
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Matches 81
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RESULT 9

PRESULT 9

PROACHO
Probable YME1 ATP-dependant proteinase [imported] - Arabidopsis thaliana
NyAlternate names: YTA11 protein homolog T19118.5
C.Species: Atablodpsis thaliana (mouse-ear cress)
C.Accession: T0520; Had&Sc.
Everysion 24-Mar-1999 #text_change 09-Jul-2004
R.Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMB1 Data Library, August 1998
A.Pescription: Arabidopsis thaliana chromosome II BAC T19118 genomic sequence.
A.Reference number: Z14681
A.Rolcule type: DNA
A.Resion: T0521
A.Rolcule type: DNA
A.Resion: T0527 cROU-
A.Roos-references: UNIRROR:080983; EMB1.AC004747; NID:g3413696; PID:g3413700
A.Roos-references: UNIRROR:020983; EMB1.AC004747; NID:g3413696; PID:g3413700
A.Roos-references: UNIRROR:020093; EMB1.AC004747; NID:g3413696; PID:g3413700
A.Roos-reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MuID:20083487; PMID:10617197
A.Roos-reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487; PMID:10617197
A.Roos-references: GB:AE002093; NID:g3413700; PIDN:AAC31223.1; GSPDB:GN00139
A.Genetics: Preliminary
A.Roos-references: GB:AE002093; NID:g3413700; PIDN:AAC31223.1; GSPDB:GN00139
A.Genetics: 19218.5
A.Genetics: 40/1: 119/1: 160/3; 319/3
A.Rubricon: 2
A.Rubricon: 40/1: 119/1: 160/3; 319/3
C.Superfamily: cell division protein ftsH; PtsH/SEC18/CDC48-type ATP-binding domain homo
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A56038
DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C; Accession: A56038
R; Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
Mol. Cell. Biol. 14, 6809-6818, 1994
A; Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaste
A; Reference number: A56038; MUID:95021209; PMID:7935398
A; Reference number: A56038
A; Reference number: A56038
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     A; Cross-references: GB:D14637; NID:g391768; FIDN:BAA034
C; Genetics:
A; Gene: PEBP2alphaA
C; Superfamily: transcription factor CBF alpha 2
C; Keywords: alternative splicing; DNA binding; T-cell;
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Pred. No. 4.3e
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N;Alternate names: PEA2 alpha chain type 1; PEA2 alpha chain type 2; PEBP2 alpha
C;Species: Mus musculus (house mouse)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A48233; B4823
R;Ogawa, E.; Maruyama, M.; Kagoshima, H.; Inuzuka, M.; Lu, J.; Satake, M.; Shige
Proc. Natl. Acad. Sci. U.S.A. 90, 6889-6863, 1993
A;Title: PEBP2/PEA2 represents a family of transcription factors homologous to t
A;Reference number: A48233; MUID:93342088; PMID:8341710
A;Accession: A48233
A;Accession: B48233
A;Cross-references: UNIPROT:Q08775; GB:D14636; NID:g391766; PIDN:BAA03485.1; PID
A;Accession: B48233
A;Accession: B48233
A;Accession: B48233
A;Residues: 1-304,'L',306 <OG2>
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$31223
transcription factor Brn-1 - mouse
NyAlternate names: class III POU domain protein brain-1
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2
C;Accession: $31223
C;Accession: $31223
R;Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M.
Froc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A;Title: Structure and evolution of four POU domain genes expressed in m A;Reference number: $31223; MUID:92228768; PMID:1565620
A;Reference number: $31223; MUID:92228768; PMID:1565620
A;Reference: UNA
A;Residues: 1-495 cHAR>
A;Residues: 1-495 cHAR>
A;Residues: 11-27 cHAR>
A;Residues: UNIPROT:P31361; EMBL:W88299; NID:g200444; PIDN:AAA35
C;Superfamily: transcription factor Brn-1; homeobox homology; POU domain: C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;101-112/Region: glycine-rich
F;162-180/Region: alanine-rich
F;236-247/Region: glycine-rich
F;236-247/Region: glycine-rich
F;236-247/Region: glycine-rich
F;236-247/Region: glycine-rich
F;246-291/Region: histidine/proline-rich
F;36-383/Domain: POU domain homeology <a href="https://docentrol.com/">homeobox homology <a href="https://doc
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No.
                                                         A; Cross-references: GDB:136411; OMIM:142994
A; Map position: 1g41-1g42.1
C; Superfamily: unassigned homeobox proteins
C; Keywords: DNA binding; homeobox; nucleus;
F; 244-300/Domain: homeobox homology <HOX>
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ribosomal protein L14 - human
C; Species: Homo sapiens (man)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-C; Accession: JC5954
C; Accession: JC5954
R; Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A; Title: Triplet repeat-containing ribosomal protein L14 gene in im A; Reference number: JC5954; MUID: 98153799; PMID: 9480843
A; Accession: JC5954
A; Accession: JC5954
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-220 < TAN>
A; Residues: 1-220 < TAN>
C; Superfamily: rat ribosomal protein L14
C; Superfamily: rat ribosomal protein L14
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Pred. No. 1.7e-05;
0; Mismatches 0;
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2
C;Accession: T13748
R;Sinclair, D.A.R.; Milne, T.A.; Hodgson, J.W.; Shellard, J.; Salinas, C
Development 125, 1207-1216, 1998
A;Title: The Additional sex combs gene of Drosophila encodes a chromatin
A;Reference number: Z17750; MUID:98146384; PMID:9477319
A;Accession: T13748
A;Accession: T13748
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1668 <SIN>
A;Cross-references: EMBL:AJ001164; NID:93292938; PIDN:CAA04568.1; PID:932
C;Genetics:
A;Cross-references: FlyBase:FBgn0000142
C;Function:
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C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul
C;Accession: S16356
R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A;Title: The ovo gene of Drosophila encodes a zinc finger protein requ
A;Reference number: S16356; MUID:91293102; PMID:1712294
A;Accession: S16356
A;Accession: S16356
A;Accession: S16356
A;Accession: S16356
A;Accession: S16356
A;Cross-references: UNIPROT:Q8T8L9; EMBL:X59772
C;Genetics:
A;Gene: FlyBase:ovo
A;Cross-references: FlyBase:FBgn0003028
A;Introns: 931/3; 1152/3
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                                                                                                             Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; head 8.9e-06;
                                                                                                             Score 16; DB 2; Losted. No. 7.7e-06; D; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB; Pred. No. 8.90; Mismatches
               C;Genetics:
A;Gene: ovo
A;Cross-references: FlyBase:FBgn0003028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.3%; Scu
100.0%; Pr
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100.0%; P3
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Matches 16; Conservative
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Best Local S
Matches 16
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Best Local
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Length

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DB

Score 15;

3.1%;

Query Match

RESULT JC5954

PID:9669105

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evolution

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RESULT 15
T14911

DZIP DNA-binding protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #text_change 09-Jul-2004
Not. Gen. Genet. 257, 555-605, 1998
A;Title: CPRF44, a novel plant bZIP protein of the CPRF family: comparative analysis of A;Accession: T14911
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Coss: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: MRNA
A;Residues: 1-420 ~kIR>
C;Genteins: J-420 ~kIR>
A;Coss-references: UNIPROT:082037; EMBL:Y10810; NID:g3336904; PIDN:ChA71770.1; PID:g333
C;Genteince: CPRF4b
C;Genteince: CPRF4b
C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
C;Keywords: DNA binding; leucine zipper
                                              .
0
                                              Gaps
                                              0
                                          Indels
       Pred. No. 2.8e-05; Mismatches 0;
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels

397 PAAAAAAAAAAAA 411

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20:15:07

2004,

Search completed: December 15, Job time: 41 secs

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